

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:19:36 ; Search time 16 Seconds

(without alignments)
914.482 Million cell updates/sec

Title: US-10-662-431-2

Perfect score: 1478

Sequence: 1 MAMMEVQGSPSLGQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1478	100.0	281	1	TN10_HUMAN P50591 homo sapien
2	930	62.9	291	1	TN10_MOUSE P50592 mus musculu
3	267.5	18.1	318	1	TN11_RAT Q9592 r tumor nec
4	258.5	17.5	316	1	TN11_MOUSE Q35235 m tumor nec
5	251.5	17.0	317	1	TN11_HUMAN O14788 h tumor nec
6	189.5	12.8	279	1	TNF6_MOUSE P41047 mus musculu
7	187	12.7	280	1	TNF6_CERTO Q9bdl1 cercocebus
8	186	12.6	281	1	TNF6_HUMAN P48023 homo sapien
9	185	12.5	280	1	TNF6_MACMU Q9myl6 macaca mula
10	184	12.4	272	1	TNF6_CHICK Q918d8 gallus gall
11	182	12.3	282	1	TNF6_PIG Q9bea8 sus scrofa
12	177.5	12.0	278	1	TNF6_RAT P36940 rattus norv
13	164	11.1	261	1	TNF5_BOVIN P51749 bos taurus
14	160	10.8	174	1	TN15_HUMAN O95150 homo sapien
15	159.5	10.8	240	1	TN14_MOUSE O43557 homo sapien
16	152.5	10.3	239	1	TN14_MOUSE Q9qyh9 mus musculu
17	152	10.3	261	1	TNF5_CAIJA Q9bdl3 callithrix
18	150.5	10.2	261	1	TNF5_AOTTR Q9bdl3 aotus trivi
19	149.5	10.1	260	1	TNF5_FELCA Q97605 felis silve
20	148	10.0	261	1	TNF5_MACMU Q9bdc7 macaca mula
21	147.5	10.0	260	1	TNF5_CANFA O97626 canis famil
22	147.5	10.0	261	1	TNF5_HUMAN P29965 homo sapien
23	143	9.7	261	1	TNF5_PIG Q95mq5 sus scrofa
24	140	9.5	260	1	TNF5_MOUSE P27548 mus musculu
25	136.5	9.2	235	1	TNFA_RABIT P04924 oryctolagus
26	135	9.1	229	1	TNFA_CEREL P51743 cervus elap
27	134.5	9.1	204	1	TNFB_PIG P26445 sus scrofa
28	134	9.1	234	1	TNFA_BOVIN P59684 bos indicus
29	133.5	9.0	260	1	TNFB_RAT Q9z2v2 rattus norv
30	133	9.0	232	1	TNFA_PIG P23563 sus scrofa
31	133	9.0	234	1	TNFA_CAVPO P51435 cavia porce
32	131.5	8.9	233	1	TNFA_BUBBU P59693 bubalus bub
33	131.5	8.9	233	1	TNFA_PAPSP P33620 papio sp. (

34	131	8.9	234	1	TNFA_HORSE P29553 equus cabal
35	131	8.9	253	1	TNFA_SPRAU Q9jfg3 sparus aura
36	130.5	8.8	233	1	TNFA_BOVIN Q06599 bos taurus
37	129.5	8.8	235	1	TNFA_PERLE P36939 peromyscus
38	127.5	8.6	204	1	TNFB_BOVIN Q06600 bos taurus
39	127.5	8.6	233	1	TNFA_MARMO Q35734 marmota mon
40	125.5	8.5	233	1	TNFA_HUMAN P01375 homo sapien
41	123.5	8.4	235	1	TNFA_MOUSE P06804 mus musculu
42	123.5	8.4	235	1	TNFA_PANTR P16599 rattus norv
43	122	8.3	205	1	TNFB_HUMAN P01374 homo sapien
44	122	8.3	232	1	TNFA_PANTR Q9hzd9 pan troglod
45	122	8.3	234	1	TNFA_CAPHI P13296 capra hircu

ALIGNMENTS

RESULT 1	TN10_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
GN	TNFSF10 OR TRAIL OR APO2L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96111955; PubMed=8777713;			
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF			
RT	family that induces apoptosis.";			
RL	Immunity 3:673-682(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96278649; PubMed=8663110;			
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,			
RA	Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor			
RT	necrosis factor cytokine family.";			
RL	J. Biol. Chem. 271:12687-12690(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

RN [4] X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RP MEDLINE=20017054; PubMed=10549288;
RX Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed=10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RT Jones E.Y., Sreaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
RX MEDLINE=99413670; PubMed=10485660;
RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
RA Sung Y.C., Oh B.-H.;
RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
RT selective antitumor activity.";
RL Immunity 11:253-261(1999).
CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
CC trimer.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC AND PROSTATE.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; U37518; AAC50332.1; -.
DR EMBL; U57059; AAB01233.1; -.
DR EMBL; BC032722; AAH32722.1; -.
DR PDB; 1D0G; 22-OCT-99.
DR PDB; 1D4V; 01-NOV-99.
DR PDB; 1D2Q; 11-FEB-00.
DR PDB; 1D6F; 26-SEP-01.
DR Genew; HGNC:11925; TNFSF10.
DR MIM; 603598; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; I.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KM Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
KW Zinc; 3D-structure.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 39 281 (POTENTIAL).
FT METAL 230 230 EXTRACELLULAR (POTENTIAL).
FT STRAND 123 127 ZINC.
FT TURN 130 131
FT TURN 137 139
FT STRAND 149 150
FT STRAND 163 165
FT STRAND 167 170
FT TURN 171 172
FT STRAND 173 176
FT STRAND 180 193
FT STRAND 205 213
FT STRAND 220 228
FT STRAND 237 250
FT TURN 252 253
FT STRAND 255 260
FT HELIX 263 265
FT STRAND 266 267
FT TURN 270 272
FT STRAND 274 281
SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 1478; DB 1; Length 281;
Best local Similarity 100.0%; Pred. No. 8e-115;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMEVQGGPSLGQTCVLLIVFTVLLQSLCYAVTVYVFTNELKQMDKYSKGIACFLKE 60
Db 1 MAMEVQGGPSLGQTCVLLIVFTVLLQSLCYAVTVYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQRLQRLVRKMLLTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DSYWDPNDEESMNSPCWQVKQRLQRLVRKMLLTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQMVYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQMVYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240
QY 241 SIYQGI FELKENDRI FVSVTNEHLIDMDHEASFE GAFLVG 281
Db 241 SIYQGI FELKENDRI FVSVTNEHLIDMDHEASFE GAFLVG 281

RESULT 2
TN10 MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein).
GN TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9611955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis.";
RL Immunity 3:673-682(1995).
CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

```

CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: WIDESPREAD.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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C		EMBL; U37522; AAC52345.1; --.	
D	DR	HSSP; P50591.; IDOG.	
D	DR	MGD; MGI:107414; Tnfsef10.	
D	DR	InterPro; IPR006052; TNF_family.	
D	DR	InterPro; IPR008983; TNF_like.	
D	DR	InterPro; IPR003636; TNF_subf.	
D	DR	Pfam; PF00229; TNF; 1.	
D	DR	Prodrom; PD002012; TNF_subf; 1.	
D	DR	SMART; SM00207; TNF; 1.	
D	DR	PROSITE; PS00251; TNF_1; 1.	
D	DR	PROSITE; PSS0049; TNF_2; 1.	
K	KW	Cytokine; Transmembrane; Signal-anchor; Apoptosis.	
F	FT	DOMAIN	1 17 CYTOPLASMIC (POTENTIAL).
F	FT	TRANSMEM	18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
F	FT	DOMAIN	39 291 EXTRACELLULAR (POTENTIAL).
F	FT	CARBOHYD	52 52 N-LINKED (GLCNAC....) (POTENTIAL).
S	SQ	SEQUENCE	291 AA; 33477 MW; 3FEACAB9FD7DD802 CRC64;

Query Match	62.9%;	Score 930;	DB 1;	Length 291;
Best Local Similarity	65.6%;	Pred. No. 1.4e-69;		
Matches 177;	Conservative 37;	Mismatches 50;	Indels 6;	Gaps 1;

[illegible]

RESULT 3	TN11_RAT	TN11_RAT	STANDARD;	PRT;	318 AA.
ID	TN11_RAT				
AC	Q9ESE2; Q9IZI9;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator				
DE	of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-				
DE	induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast				
DE	differentiation factor) (ODF).				
GN	TNFSF11 OR RANKL OR TRANCE OR OPGL.				

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tibial bone;
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
RN [2]
RP SEQUENCE OF 266-318 FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=21662371; PubMed=11804028;
RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A.,
RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA Marks S.C. Jr.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the TNFSF11 (TRANCE, RANKL, ODF, OPG) gene.";
RL Int. J. Dev. Biol. 45:853-859(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/ODG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC
DR EMBL; AF187319; AAG17031.1; -.
DR EMBL; AF425669; AAL23963.1; -.
DR HSSP; P50591; 1D0G.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT CHAIN 1 318
FT
FT CHAIN 141 318
FT
FT DOMAIN 1 47
FT TRANSMEM 48 68
FT
FT DOMAIN 69 318
FT SITE 140 141
FT CARBOHYD 199 199
FT CARBOHYD 264 264
FT CONFLICT 317 317
SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD09BF CRC64;

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FT	CHAIN	1	318	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 11, MEMBRANE FORM.
FT	CHAIN	141	318	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 11, SOLUBLE FORM.
FT	DOMAIN	1	47	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	48	68	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT				EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	69	318	CLEAVAGE (BY SIMILARITY).
FT	SITE	140	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	199	264	I -> M (IN REF. 2).
FT	CARBOHYD	264	317	
FT	CONFLICT	317		
SO	SEQUENCE	318 AA:	35370 MW:	4B87A4D706AD098F CRC64:


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Query Match      18.1%; Score 267.5; DB 1; Length 318;
Best Local Similarity 27.3%; Pred. No. 8e-15;
Matches 82; Conservative 55; Mismatches 106; Indels 57; Gaps 11;

QY 10 PSLGQTCVLIVITVLLQSLCAVATYVYFTNELKQMDKYSKSGIACF-----LKED--- 61
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 43 PAASRFEMFLALLGLGQVVCISALFLYFRAQMD--PNRISEDSTRCFYRILRLRENTGL 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 62 -DSYMDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISVQOEKQONISPLVRERGPQ 120
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 101 QDSTLESEDTLEALPDCSRMKQAFQ-----GAVQRELQHV-----GPQ 139
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 121 R---VAAHITGT-----RGRS-----NTLSSPNSKNEKALGRKINSWESSRSGH 161
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 140 RFGGVPAAMEGSMWLDVARRGKPEAQFPAHLTINADIPSGSHKVSU-----SSWYHDR-GW 194
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 162 SFLSNLHRLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKYT-SYDPPI 220
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 195 AKISNMTLSNGKLRVNQDGFYLYANICFRHETSGSVPADYQLMWYVVKTSIKIPSSH 254
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 221 LLMKSARNSCWSKDAEYGLYSITYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLV 280
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 255 NLMKGGSTKXWNSGNSEHFYSINVGGEFKLRAGEEISVQVSNPSLLDDPDATYFGAFKV 314
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 4
TN11_MOUSE      STANDARD;      PRT;      316 AA.
ID TN11_MOUSE
AC 035235; 035306; Q9JUK8; Q9JUK9; Q9R1Y0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
DE (OCIF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
   [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RA "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RA that activates c-Jun N-terminal kinase in T cells.";
RA J. Biol. Chem. 272:25190-25194(1997).
   [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymic lymphoma;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
RA and dendritic-cell function.";
RA Nature 390:175-179(1997).
   [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast
```

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RT differentiation and activation.";
RL Cell 93:165-176(1998).
   [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow stroma;
RX MEDLINE=98188248; PubMed=9520411;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RA "Osteoclast differentiation factor is a ligand for
RA osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RA to TRANCE/RANKL.";
RA Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
   [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=129;
RX MEDLINE=99214075; PubMed=10196481;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RA "Cloning and characterization of the gene encoding mouse osteoclast
RA differentiation factor.";
RA Gene 230:121-127(1999).
   [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21150053; PubMed=11250921;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RA "Determination of three isoforms of the receptor activator of nuclear
RA factor-kappaB ligand and their differential expression in bone and
RA thymus.";
RA Endocrinology 142:1419-1426(2001).
   [7]
RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX MEDLINE=99240759; PubMed=10224132;
RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
RA "Evidence for a role of a tumor necrosis factor-alpha
RA (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a
RA TNF family member involved in osteoclastogenesis and dendritic cell
RA survival.";
RA J. Biol. Chem. 274:13613-13618(1999).
   [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX MEDLINE=21464816; PubMed=11581298;
RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RA "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RA of receptor-ligand specificity.";
RA J. Clin. Invest. 108:971-979(2001).
   [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX MEDLINE=21839021; PubMed=11733492;
RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RA "Crystal structure of the extracellular domain of mouse RANK ligand at
RA 2.2-A resolution.";
RA J. Biol. Chem. 277:6631-6636(2002).
   [10]
RP FUNCTION: Cytokine that binds to TNFSF11B/OPG and to
RP TNFSF11A/RANK. Osteoclast differentiation and activation factor.
RP Augments the ability of dendritic cells to stimulate naive T-cell
RP proliferation. May be an important regulator of interactions
RP between T cells and dendritic cells and may play a role in the
RP regulation of the T cell-dependent immune response. May also play
RP an important role in enhanced bone-resorption in humoral
RP hypercalcemia of malignancy.
   [11]
RP SUBUNIT: Homotrimer.
RP -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted
RP (isoforms 1 and 2); Cytoplasmic (isoform 3).
RP -1- ALTERNATIVE PRODUCTS:
RP Event=Alternative splicing; Named isoforms=3;
RP Name=1;
RP IsoId=O35235-1; Sequence=Displayed;
RP Name=2;
RP IsoId=O35235-2; Sequence=VSP_006449;
RP Name=3;
RP IsoId=O35235-3; Sequence=VSP_006448;
```


CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC TRABECULAR BONE AND LUNG.
CC -1- PTM: N-glycosylated.
CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing. The cleavage may be catalyzed by
CC ADAM17. A further shorter soluble form was observed.
CC -1- DISEASE: Deficiency in TNFSF11 results in failure to form lobulo-
CC alveolar mammary structures during pregnancy, resulting in death
CC of newborns. Trance-deficient mice show severe osteopetrosis, with
CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC profound growth retardation at several skeletal sites, including
CC the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC with thick, irregular growth plates and a relative increase in
CC hypertrophic chondrocytes.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; AF013170; AAC71061.1; -.
DR EMBL; AF019048; AAB86812.1; -.
DR EMBL; AF053713; AAC40113.1; -.
DR EMBL; AB008426; BAA25425.1; -.
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR EMBL; AB032771; BAA97257.1; -.
DR EMBL; AB032772; BAA97258.1; -.
DR EMBL; AB036798; BAA97259.1; -.
DR PDB; 1J7Z; 28-JAN-03.
DR PDB; 1IOA; 14-JAN-03.
DR MGD; MGI:1100089; Tnfsf11.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0001503; P:ossification; IMP.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; 3D-structure; Alternative splicing.
FT CHAIN 1 316
FT CHAIN 139 316
FT DOMAIN 1 48
FT TRANSMEM 49 69
FT DOMAIN 70 316
FT SITE 138 139
FT CARBOHYD 197 197
FT CARBOHYD 262 262
FT VARSPLIC 1 117
FT VARSPLIC 14 44
FT CONFLICT 99 99
FT CONFLICT 141 143
FT STRAND 164 169
FT TURN 171 172
FT STRAND 181 182

FT STRAND 186 187
FT TURN 191 192
FT STRAND 194 196
FT STRAND 198 201
FT TURN 202 203
FT STRAND 204 207
FT STRAND 211 224
FT HELIX 225 227
FT STRAND 234 245

Query Match 17.5%; Score 258.5; DB 1; Length 316;
Best local Similarity 26.4%; Pred. No. 4.4e-14;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 10 PSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACF-----LKEDDSY 64
Db 43 PAASRSMTLALLGLGLGVVCSIALFLYFRAQMD--PNRISEDSTHCFYRLRLHENAGL 100

QY 65 WDP--NDEESMNSPCWQVKWQLRQLVYRKMLRTSEFTISTVDEKQONISPL----- 113
Db 101 QDSTLESDTLPDSCRRMKQAFQGAVOK-----ELQHTVGFQRFSGAPAMM 146

QY 114 -----VREKGPQVVA--AHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
Db 147 EGSWLDVAQRGKPEAQPFAPHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196

QY 166 NMLHRLNGELVTHEKGFYYIYSGTYFRFQEEIKENTKNDKQWQYIYKYT-SYDPILIMK 224
Db 197 NMTLSNGKLRVNQDGFYLLYANICERHNETSGSVPTDYQLMYVYVYKTSIKIPSSHNLMK 256

QY 225 SARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLV 280
Db 257 GGSSTKWSGNSEFHFYSINVGFFKLRAGEEISIQVSNPSLDDPDQDATYFGAFKV 312

RESULT 5
TN11_HUMAN
ID TN11_HUMAN STANDARD; PRT; 317 AA.
AC O14788; O14723; Q96Q17; Q9P2Q3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Bone marrow, and Peripheral blood;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lymph node;
RX MEDLINE=98227661; PubMed=9568710;
RA lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).

```

RP [3] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RA Ikeda T., Kuroyama H., Hirokawa K.;
RT "Determination of human RANKL isoforms.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 73-317 FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalchikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Tongue;
RX MEDLINE=20175237; PubMed=10708588;
RA Nagai M., Kyakumoto S., Sato N.;
RT "Cancer cells responsible for humoral hypercalcemia express mRNA
RT encoding a secreted form of ODF/TRANCE that induces osteoclast
RT formation.";
RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1B/ODG and to
CC TNFRSF1A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC Secreted (isoform 2). A soluble form of isoform 1 arises by
CC proteolytic processing (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=O14788-1; Sequence=Displayed;
CC Name=2; Synonyms=SODF;
CC IsoId=O14788-2; Sequence=VSP_006447;
CC Name=3;
CC IsoId=O14788-3; Sequence=VSP_006446;
CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
CC IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing (By similarity). The cleavage may be
CC catalyzed by ADAM17.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
CC EMBL; AF019047; AAB86811.1; -
CC EMBL; AF053712; AAC39731.1; -
CC EMBL; AB064269; BAB79694.1; -
CC EMBL; AB061227; BAB71768.1; -
CC EMBL; AB064270; BAB79695.1; -
CC EMBL; AF013171; AAC51762.1; -
CC EMBL; AB037599; BAA90488.1; -
CC HSSP; P50591; 1D0G.
CC Genew; HGNC:11926; TNFSF11.
CC MIM; 602642; -
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0005887; C:integral to plasma membrane; NAS.

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DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	GO; GO:0030316; P:osteoclast differentiation; NAS.			
DR	InterPro; IPR006052; TNF_family.			
DR	InterPro; IPR008983; TNF_like.			
DR	InterPro; IPR003636; TNF_subf.			
DR	Pfam; PF00229; TNF; 1.			
DR	ProDom; PD002012; TNF_subf; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; FALSE_NEG.			
DR	PROSITE; PS50049; TNF_2; 1.			
KW	Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Alternative splicing.			
FT	CHAIN	1	317	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, MEMBRANE FORM.
FT	CHAIN	140	317	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN	1	47	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	48	68	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	69	317	EXTRACELLULAR (POTENTIAL).
FT	SITE	139	140	CLEAVAGE (BY SIMILARITY).
FT	CARBOHYD	171	171	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	1	47	Missing (in isoform 3).
FT	VARSPPLIC			/FTid=VSP_006446.
FT	VARSPPLIC	1	73	Missing (in isoform 2).
FT	VARSPPLIC			/FTid=VSP_006447.
FT	CONFLICT	194	194	A -> G (IN REF. 4).
FT	SEQUENCE	317 AA;	35478 MW;	766176446348097F CRC64;

Query Match	17.0%;	Score 251.5;	DB 1;	Length 317;
Best Local Similarity	24.1%;	Pred. No. 1.7e-13;		
Matches 71;	Conservative	61;	Mismatches 117;	Indels 45;
				Gaps 10;

QY	10	PSLGÖTCVLIVIFTVLLQSLCVAATVYVFTNELKÖMÖDKYSKSGIACF----	IKED----	61
		: : : : : : : : : : : : : : :		
Db	42	PASRSMFVALLGLGÖVVCVVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF		99
QY	62	-DSYWDPNDEESMNSPCWÖVKW-----ÖLRÖLVRKMILRTSEITI----	STVÖEKÖ	107
		: : : : : : : : : : : : : :		
Db	100	QDTTLESQDTKLIPDSCRRIKÖAFÖGAVÖKELÖHIVGSÖHIRAEKAMVDGSMWDLAKRSK		159
QY	108	ÖNISPLVBERGPÖRVAAHITGTGRSNTLLSSPNSKNEKALGRKINSWESSRSGHSFLSNL		167
		: : : : : : : : : : : : : :		
Db	160	LEAÖPF-----AHLT-----INATDIPSGSHKVSL---SSWYHDR-GWAKISNM		199
QY	168	HURNGELVIEHEKGFYIYSÖTYFRFÖEIKENTKNDKÖWÖYIYKYT-SYDPDILMKSA		226
		: : : : : : : : : : : : : : : :		
Db	200	TFSNGKLIVNÖDGFYLLYANICFRKHETSGLDLEYLÖLMVYVTKTSIKIPSHILMKGG		259
QY	227	RNSCWSKDAEYGLYSIYÖGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV		280
		: : : : : : : : : : : : : : : :		
Db	260	STYKWSGNSEFHFYISINVGGFFKLRSGEHISIEVSNPSLLDPDÖDÄTYFGAFKV		313

```

RESULT 6
TNF6_MOUSE
ID TNF6_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
DE TNFSF6 OR FASL OR APT1LG1 OR GLD.
GN TNFSF6 OR FASL OR APT1LG1 OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;

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RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN=BALB/c;
RA Fenner M.H., Shioda T., Isselbacher K.J.;
RT "Musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM FASLS).
RC STRAIN=C3H; TISSUE=Spleen;
RX MEDLINE=20021694; PubMed=10552956;
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
RA Cammarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene";
RL Blood 94:3456-3467(1999).
RN [6]
RP CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE=96091792; PubMed=7495745;
RA Hahne M., Peitsch M.C., Immler M., Schroeter M., Lowin B.,
RA Rousseau M., Bron C., Remo T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice.";
RL Int. Immunol. 7:1381-1386(1995).
RN [7]
RP VARIANTS ALA-184 AND GLY-218.
RC STRAIN=C57BL/6, C3H, MRL, SJL, NOD, NZB, NZW, BALB/c, DBA/1, and
RC DBA/2;
RX MEDLINE=97268671; PubMed=9108079;
RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA Yagita H.;
RT "Polymorphism of murine Fas ligand that affects the biological
RT activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
RN [8]
RP FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
RC transduces the apoptotic signal into cells. May be involved in
RX cytotoxic T cell mediated apoptosis and in T cell development.
RA TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
RA peripheral tolerance, in the antigen-stimulated suicide of mature
RT T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
RL modulates its effects (By similarity).
RN [9]
RP SUBUNIT: Homotrimer (Probable).
RX SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
RA secreted (isoforms FASL and FASLS).
RT [10]
RL ALTERNATIVE PRODUCTS:
RN [11]
RP Event=Alternative splicing; Named isoforms=2;
RC Name=FasL;
RX IsoId=P41047-1; Sequence=Displayed;
RA Name=FasLS;
RX IsoId=P41047-2; Sequence=VSP_006445;
RA PTM: The soluble form derives from the membrane form by
RT proteolytic processing (By similarity).
RL [12]
RP DISEASE: A deficiency in this protein is the cause of generalized

CC lymphoproliferation disease phenotype (Gld). Gld mice present
CC lymphadenopathy and autoantibody production. The phenotype is
CC recessively inherited.
CC
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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DR	EMBL; U06948; AAA17800.1; -.
DR	EMBL; U10984; AAA19778.1; -.
DR	EMBL; S76752; AAB33780.1; -.
DR	EMBL; U58995; AAB02915.1; -.
DR	EMBL; AF119335; AAD52106.1; -.
DR	PIR; A53062; A53062.
DR	HSSP; P01375; ATSV.
DR	MGD; MGI:99255; Tnf α f6.
DR	InterPro; IPR008064; Fas_ligand.
DR	InterPro; IPR006053; TNF_abc.
DR	InterPro; IPR006052; TNF_family.
DR	InterPro; IPR008983; TNF_like.
DR	InterPro; IPR003636; TNF_subf.
DR	Pfam; PF00229; TNF_1.
DR	PRINTS; PR01681; FASLIGAND.
DR	PRINTS; PR01234; TNECROSISFCT.
DR	ProDom; PD002012; TNF_subf; 1.
DR	SMART; SM00207; TNF_1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS50049; TNF_2; 1.
KW	Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KM	Disease mutation; Polymorphism; Alternative splicing.
FT	CHAIN 1 279
FT	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM.
FT	CHAIN 128 279
FT	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT	CYTOPLASMIC (POTENTIAL).
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL).
FT	POLY-RICH.
FT	POLY-PRO.
FT	CLEAVAGE (BY SIMILARITY).
FT	POTENTIAL.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	Missing (in isoform FaSLs).
FT	/FTid=VSP_006445.
FT	T -> A (IN STRAINS BALB/C AND DBA; ENHANCES CYTOTOXICITY).
FT	E -> G (IN STRAINS BALB/C AND DBA; ENHANCES CYTOTOXICITY).
FT	F -> L (IN GLD; ABOLISHES BINDING OF FAST TO ITS RECEPTOR).
FT	SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;

```

Query Match          12.8%; Score 189.5; DB 1; length 279;
Best Local Similarity 25.8%; Pred. No. 1.9e-08;
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY      83 QLRQLVRKMILRTSEETISTVQEKQNISPLVREKGPQRYAAHITGTRGRSNTLLSPNSK 142
       :|||:   : : : : : ||| : : ||| : ||| : ||| : : ||| :
Db      111 ELRFFTNQSL-----KVSSFEKQIANPSTPSEKEKPRSV-AHLTG-----NPHSR 154

QY      143 NEKALGRKINSWESSRSRGSHFLSNLHLRNGELVIHEKGFYYIYSQTYFRFOEIKENTKN 202
       : || : | : : : : : | ||| : | | : : ||| : ||| : |
Db      155 SIPL-----EMEDT-YGTALISGVKKYKKGGGLVINETGLTVFVYSKYVFRGQ-----SCN 201

```


[illegible]

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB 261
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RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206, TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228058;
RA Schneider P., Bodmer J.-L., Holler N., Matmann C., Scuderi P.,
RA Terstikh A., Peltsch M.C., Tschopp J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998).
RN [11]
RP FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
modulates its effects.
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
into the extracellular fluid, probably by cleavage form the cell
surface.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC FT

CC ISOId=P48023-1; Sequence=Displayed;
CC Name=2;
CC ISOId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form derives from the membrane form by
proteolytic processing.
CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
involving hemolytic anemia and thrombocytopenia with massive
lymphadenopathy and splenomegaly.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
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CC -----

CC EMBL; X89102; CAA61474.1; -
CC EMBL; U08137; AAC50071.1; -
CC EMBL; U11821; AAC50124.1; -
CC EMBL; D38122; BAA07320.1; -
CC EMBL; AF288573; AAG60017.1; -
CC EMBL; Z96050; CAB09424.1; -
CC EMBL; BC017502; AAH17502.1; -
CC EMBL; AB013303; BAA32542.1; -
CC PIR; I38707; I38707.
CC HSSP; P01375; 1TNF.
CC Genew; HGNC:11936; TNFSF6.
CC MIM; 134638; -
CC MIM; 601859; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008064; Fas_ligand.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01681; FASLIGAND.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW Alternative splicing; Antigen.
CC CHAIN 1 281
CC FT
CC CHAIN 130 281
CC FT
CC DOMAIN 1 80
CC TRANSMEM 81 102
CC FT
CC DOMAIN 103 281
CC DOMAIN 4 70
CC DOMAIN 45 65
CC SITE 129 130
CC DISULFID 202 233
CC CARBOHYD 184 184
CC CARBOHYD 250 250
CC CARBOHYD 260 260
CC VARSPPLIC 117 127
CC FT
CC FTId=VSP_006443.
CC

FT VARSPIC 128 281 Missing (in isoform 2).
FT FTID=VSP 006444.
FT MUTAGEN 206 206 P->D,F,R: LOWERS BINDING TO TNFRSF6 AND
FT REDUCES CYTOTOXICITY MORE THAN 100-FOLD.
FT MUTAGEN 218 218 Y->F,R: LOWERS BINDING TO TNFRSF6 AND
FT ABOLISHES CYTOTOXICITY.
FT MUTAGEN 275 275 F->L: ABOLISHES BINDING TO TNFRSF6 AND
FT CYTOTOXICITY.
SQ SEQUENCE 281 AA, 31485 MW, A8A6EB358246E9B CRC64;
Query Match 12.6%; Score 186; DB 1; Length 281;
Best Local Similarity 22.1%; Pred. No. 3.6e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;
QY 4 MEVGGPSLQGTCLVIFVTLVQLVAV--TYVFTNELKQMDKYSKGIACFLKE 60
DB 71 LKRGHSTG-LCLVWFVWLVALVGLGMFQLFHLQKELARESTSQMHTASSDEK 129
QY 61 DDSYMDPNDESMNSPCWQVKQLRLVRKMLRTSEFTISTVQEKQONISPLVRERGPQ 120
DB 130 QIGHPSPPPE-----KKELRKV----- 146
QY 121 RVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
DB 147 ---AHLT---GKSNSRSM-----LEWEDT-YGIVLLSGVKYKKGGVLINETG 187
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIY-KYTSYDPILMKSAKNS-----CWSK 233
DB 188 LYFVYSKYVFRGQ-----SCNNPLSHKVMYRNKSKYPQDLVMEGKMSYCTTGQWMAW 241
QY 234 DAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
DB 242 -----SYLGAVENLTSADHLVYVNSLSLVNFESQTFFGLY 279
RESULT 9
TNF6_MACMU STANDARD; PRT; 280 AA.
ID TNF6_MACMU
AC Q9MYL6; Q9BDM5; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RA Kirii Y., Inoue T., Yoshino K.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects (By similarity).

CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
CC EMBL; AF344856; AAK37539.1; -.
CC EMBL; AB035138; BAA90294.1; -.
CC EMBL; AB035139; BAA90295.1; -.
CC EMBL; AB035140; BAA90296.1; -.
CC HSSP; P01375; 4TSV.
CC InterPro; IPR008064; Fas_ligand.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01681; FASLIGAND.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC DR PROSITE; PS0049; TNF_2; 1.
CC KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 6, MEMBRANE FORM.
FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 69 PRO-RICH.
FT SITE 128 129 POLY-PRO.
FT DISULFID 201 232 CLEAVAGE (BY SIMILARITY).
FT CARBOHYD 183 183 POTENTIAL.
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 60 60 S->P (IN REF. 1).
SQ SEQUENCE 280 AA, 31367 MW, F0B284D61A132EB4 CRC64;
Query Match 12.5%; Score 185; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 4.4e-08;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;
QY 4 MEVGGPSLQGTCLVIFVTLVQLVAVTYVFTNELKQMDKYSKGIACFLKEDDS 63
DB 70 LKRGHSTG-LCLVWFVWLVALVGLGMFQLFHLQKELARESTSQMHTASSDEK 118
QY 64 YMDPNDESMNSPCWQVKQLRLVRKMLRTSEFTISTVQEKQONISPLVRERGPQ 123
DB 119 -----QKHTASSLEKQIGHPS-PPEKKEQKV 145
QY 124 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKPY 183
DB 146 AHLTG-----KPNRSMP-----EWEDT-YGIVLLSGVKYKKGGVLINETGYF 189
QY 184 IYSQTYFRFOEIKENTKNDKQWQYIY-KYTSYDPILMKSAKNSCWSKDAEYGLYSI 242
DB 190 VYSKYVFRGQ-----SCNNPLSHKVMYRNKSKYPQDLVMEGKMS-YCTTGQWMAHSS 242
QY 243 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Db 243 YLGAVENLTADHLVYVNSELSLVNFEESQTFFGLY 278

RESULT 10

TNF5_CHICK

ID TNF5_CHICK STANDARD; PRT; 272 AA.

AC Q918D8;

DT 28-FEB-2003 (Rel. 41, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L)

DE TNF5 (CD154 protein).

GN TNF5 OR CD40LG OR CD40L.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn; TISSUE=Spleen;

RA Tregaskes C.A., Young J.R., Burnside J.;

RT "Cloning of a putative chicken CD40 ligand.";

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

CC -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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DR EMBL; AJ243435; CAB95748.2; -.

DR HSSP; P29965; ITALY.

DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO; GO:0005174; F:CD40 receptor binding; ISS.

DR GO; GO:0042100; P:B-cell proliferation; ISS.

DR GO; GO:0006954; P:inflammatory response; ISS.

DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.

DR GO; GO:0030168; P:platelet activation; ISS.

DR InterPro; IPR003263; TNF_5.

DR InterPro; IPR006052; TNF_family.

DR InterPro; IPR008983; TNF_like.

DR InterPro; IPR003636; TNF_subf.

DR Pfam; PF00229; TNF_1.

DR PRINTS; PR01702; CD40LGAND.

DR ProDom; PD008600; TNF_5; 1.

DR ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

FT CHAIN 1 272

FT CHAIN 111 272

FT DOMAIN 1 23

FT TRANSMEM 24 44

FT DOMAIN 45 272

FT SITE 110 111

FT DISULFID 190 229

FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

Query Match 12.4%; Score 184; DB 1; Length 272;

Best Local Similarity 25.4%; Pred. No. 5.1e-08;

Matches 69; Conservative 48; Mismatches 119; Indels 36; Gaps 9;

QY 16 CVLIVFTVLQSLCVAVTYVYFTNELKQMDKYSKGIACFLKEDDSYDNDSESMNS 75

Db 26 CFLSVFMV--QTIGTVLFLCYLHMKMKMEVLSLNEIDYIFLRKVQKQTGEDQSTLL 83

QY 76 PCWQVKQLRQLVRKMLRTSEETISTYQEKQONISPLVRERG-----QVAAHIT 127

Db 84 DCEKVLKGFQDLQCKD--RTASEELPKFEMHKGHEPHLKSRNETSVAEKKRQPIATHLA 141

QY 128 GTRGRSNTLSSPNSKNEKALGRKINSW-ESSRSGHSFLSNLHLNGELVIHEKGFYIYS 186

Db 142 GV--KSNITV-----RVLKMWTTSTYAPTSSLISYH--EGKLKVEKAGLYIYS 185

QY 187 QTYFRPQEEIKENTKNDKQMVYIYKYTSYDPDILMK SARNSGWSKDAEYGLYSIYGG 246

Db 186 QVSF-----CTKAASAPFTLYIYLYLPMEDRLLMKGLDTHSTS-TALCELSIREGG 238

QY 247 IFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Db 239 VFELRQGDVVFVNVTSTAVVNVNGNTYFGMF 270

RESULT 11

TNF6_PIG

ID TNF6_PIG STANDARD; PRT; 282 AA.

AC Q9BEA8; Q95M04; Q95N10;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand).

GN TNFSF6 OR FASL.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OC NCBI_TaxID=9823;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21322533; PubMed=11429161;

RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;

RT "Molecular cloning, characterization, and expression of porcine Fas ligand (CD95 ligand).";

RT J. Interferon Cytokine Res. 21:305-312(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Guanxi bama miniature pig;

RA Zhu N., Young Y.;

RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RL [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoid;

RA Tsuyuki S., Kono M., Bloom E.T.;

RT "Cloning and potential utility of porcine Fas ligand: overexpression in porcine cells protects them from attack by human cytolytic cells.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;

RX MEDLINE=21653191; PubMed=11792426;

RA Moteji-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;

RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison with human gene.";

RL Mol. Immunol. 38:581-586(2002).

CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that


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FT FT DOMAIN 1 77 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT FT TRANSMEM 78 99 CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 100 278 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT DOMAIN 4 69 (POTENTIAL).
FT FT SITE 126 127 EXTRACELLULAR (POTENTIAL).
FT FT DISULFID 199 230 POLY-PRO.
FT FT CARBOHYD 116 116 CLEAVAGE (BY SIMILARITY).
FT FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match 12.0%; Score 177.5; DB 1; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.8e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVQEQQONISPLVRERGQPRVAHITGT-RGRSNTLSSPNSXNEKALGRKINSWESSR 158
Db 121 VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL-----EWEDT- 162
QY 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYRFRQEEIKENTKNDKQWQYIY-KYTSYP 217
Db 163 YGTALLISGVKKYKKGGLVINEAGLFFVYSKYVERGQ-----SCNSQPLSHKVMRNFKYP 216
QY 218 DPLIMKSAR-NSCWSKDAEYGHVYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
Db 217 GDVLMEKKILNYCTT--GQIMAHSSYLGAVENLTVA DHLIYVNISQSLINFESKTFPG 274
QY 277 AF 278
Db 275 LY 276

RESULT 13
TNF5_BOVIN STANDARD; PRT; 261 AA.
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
DE related activation protein) (TRAP) (T cell antigen GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96006582; PubMed=7590981;
RA Mertens B.E.L.C., Murtuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT and tumor necrosis factor alpha.";
RL Immunogenetics 42:430-431(1995).
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; Z48469; CAA88363.1; -.
DR PIR; S53090; S53090.
DR HSSP; P29965; 1ALY.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005174; F:CD40 receptor binding; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_1like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01702; CD40LIGAND.
DR ProDom; PD008600; TNF_5; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT FT
FT CHAIN 113 261
FT FT
FT DOMAIN 1 22
FT TRANSMEM 23 46
FT FT
FT DOMAIN 47 261
FT SITE 112 113
FT DISULFID 178 218
FT CARBOHYD 240 240
SQ SEQUENCE 261 AA; 29242 MW; 8491FEBB30A787FD CRC64;

Query Match 11.1%; Score 164; DB 1; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.2e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VQGGPSLGQTCVLIVFTVLL--QSLCAVATVYVFTNELKQMDKYKSGIACFLKEDDS 63
Db 13 VATGPPVSMK-IFMYLLTVFLITQMGSALEAVYLLHRLDKIEDERNLHEDFVFMK--T 68
QY 64 YMDPNDEESMNS--PCWQVKWQLRLVRKMLRTSEETISTVQEKQONISPLVRERGPR 121
Db 69 IQRCNKGEGLSLINCEIRSRFDLV-KDIMQNKE----VKKEKNFEMHKGDEPQ- 121
QY 122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELYIHE 178
Db 122 IAAHV-----ISEASSKTSVYLV----QW-APKGYTTLNNLVTLLENGKQLAVKR 165
QY 179 KGFYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSPYDPILLMK SARNSCMSKDAEYG 238
Db 166 QGFYIYIQVTFCSNRE---TLSQAPFIASLCLKSPSGSERILLRAANTHSSKPC--G 219
QY 239 LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
Db 220 QQSILGGVFEFLQSGASVFVAVTDPQSQVSHGTGFTSFG 257

RESULT 14
TN15_HUMAN
ID TN15_HUMAN STANDARD; PRT; 174 AA.
AC 095150;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 15 (Vascular
DE endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
DE TNPSF15 OR VEGI OR TL1.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RX MEDLINE=99091541; PubMed=9872942;
RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
RA Li L.-Y., Gentz R., Yu G.-L.;
RT "VEGI, a novel cytokine of the tumor necrosis factor family, is an
RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
RT in vivo."
RL FASEB J. 13:181-189(1999).
CC -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
CC (in vitro).
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
CC spleen, prostate, small intestine and colon.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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DR EMBL; AF039390; AAD08783.1; -.
DR HSSP; P50591; 1D0G.
DR Genew; HGNC:11931; TNFSF15.
DR MTM; 604052; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR CytoKine; Transmembrane; Glycoprotein; Signal-anchor.
KW DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
FT DISULFID 85 125 POTENTIAL.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;
Query Match 10.8%; Score 160; DB 1; Length 174;
Best Local Similarity 35.3%; Pred. No. 2.7e-06;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;
QY 154 WESSRSGHSLSN-LHLRNGELVIEHKGYYIYSQTYFRQ---EIKENTKNDK--QM 206
DB 42 WE-HELGLAFTKRNMYTNKFLIPESGDYFIYSQVTFRGMTSECEIRQAGRPNKEDSI 100
QY 207 VOYLYKYT-SYPPDILMKSAANSCKDAEYG--LVSITYOGGIFELKENDRIFVSVTN 262
DB 101 TVVITKVTDSYEPFTQLMGTKSYC-----EVGSNWFQPIYIGAMFSLQEGDKLMVNSD 155
QY 263 EHLIDMDHE-ASFFGAFLV 280
DB 156 ISLVDTYTKEDKTFFGAFL 174

RESULT 15
TN14_HUMAN STANDARD; PRT; 240 AA.
ID TN14_HUMAN
AC 043557; 075476; Q8WVF8; Q96LD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
DE mediator-ligand) (HVEM-L).
DE TNFSF14 OR LIGHT OR HVEM-L.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98122340; PubMed=9462508;
RA Mauri D.N., Ebner R., Montgomery R.I., Kochei K.D., Cheung T.C.,
RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA Ware C.F.;
RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT ligands for herpesvirus entry mediator."
RL Immunity 8:21-30(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=98438532; PubMed=9765287;
RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA Tan K.B., Dede K., Spampinato J., Silverman C., Hensley P.,
RA Diprinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA Truneh A., Young P.R.;
RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
RT growth."
RL J. Biol. Chem. 273:27548-27556(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX MEDLINE=21528948; PubMed=11673523;
RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RT "Genomic characterization of LIGHT reveals linkage to an immune
RT response locus on chromosome 19p13.3 and distinct isoforms generated
RT by alternate splicing or proteolysis."
RL J. Immunol. 167:5122-5128(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
CC decoy receptor TNFRSF6B modulates its effects. Activates NFKB,
CC stimulates the proliferation of T cells, and inhibits growth of
CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex

```
CC virus.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoform 1); Cytoplasmic (isoform 2).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43557-1; Sequence=Displayed;
CC Name=2; Synonyms=LIGHT delta-TM;
CC IsoId=O43557-2; Sequence=VSP_006452;
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC NONHEMATOPOIETIC TUMOR LINES.
CC -1- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC -1- PTM: N-glycosylated.
CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 178.
CC -----
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CC -----
DR EMBL; AF036581; AAC39563.1; -.
DR EMBL; AF064090; AAC25169.1; -.
DR EMBL; AY028261; AAK26160.1; -.
DR EMBL; BC018058; AAH18058.1; ALT_FRAME.
DR HSSP; P01375; 4TSV.
DR Genew; HGNC:11930; TNFSF14.
DR MIM; 604520; -.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006053; TNF_ab.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW Alternative splicing.
FT CHAIN 1 240
FT FT
FT CHAIN 283 240
FT FT
FT DOMAIN 1 37
FT TRANSMEM 38 58
FT FT
FT DOMAIN 59 240
FT SITE 82 83
FT DISULFID 154 187
FT CARBOHYD 102 102
FT VARSPLIC 38 73
FT FT
FT CONFLICT 120 120
FT CONFLICT 214 214
SQ SEQUENCE 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;

Query Match 10.8%; Score 159.5; DB 1; Length 240;
Best Local Similarity 23.8%; Pred. No. 4.6e-06;
Matches 53; Conservative 41; Mismatches 66; Indels 63; Gaps 9;
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QY 79 QVKQLRLVRKMLILTSSEETISTVQEKQON-ISPLVREGRGPQVAAHITGRGRSNTLS 137
Db 60 QLHWRILGEMVTRLPDGPAGSWEQLQERRSHEVNP-----AAHLTGANSSLTGS 109
QY 138 SPNSKNEKALGRKINSWESSRSRSGHFLSNLHNRNGELVIHEKGFYIYSQTYFRFQEEIK 197
Db 110 GP-----LIME-TQLGLAFLRGLSYHDGALVVTKAGYYIYSK----- 146
QY 198 ENTKNDKQMVQY-----IYKYT-SYDPPIILMKSGARNSCWSKDAFYGLY 240
Db 147 -----YQLGVCPLGLASTITHGLYKRTPRPYPELELLVSQSPCGRATSSSRVW 197
QY 241 --SIYGGIFELKENDRIFVSVTNEHLIDM-DHEASFFGAFV 280
Db 198 WDSFLLGGVVAHLEAGEEVVVRVLDRLVRLDGTGRSYFGAFMV 240
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Search completed: September 5, 2004, 09:25:01
Job time : 17 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:23:31 ; Search time 17 Seconds
(without alignments)
853.347 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGALVVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1478	100.0	281	1	US-08-670-354-2	Sequence 2, Appli
2	1478	100.0	281	3	US-08-584-031-1	Sequence 1, Appli
3	1478	100.0	281	3	US-08-780-496-1	Sequence 1, Appli
4	1478	100.0	281	3	US-08-883-086-10	Sequence 10, Appli
5	1478	100.0	281	3	US-09-320-424-2	Sequence 2, Appli
6	1478	100.0	281	4	US-09-333-593A-6	Sequence 6, Appli
7	1478	100.0	281	4	US-09-157-864-11	Sequence 11, Appli
8	1478	100.0	281	4	US-09-825-563-2	Sequence 2, Appli
9	1478	100.0	281	4	US-10-039-785-66	Sequence 66, Appli
10	1478	100.0	281	5	PCT-US96-10895-2	Sequence 2, Appli
11	1469	99.4	279	4	US-09-072-993C-3	Sequence 3, Appli
12	988	66.8	253	3	US-09-320-424-11	Sequence 11, Appli
13	988	66.8	253	4	US-09-825-563-11	Sequence 11, Appli
14	988	66.8	256	3	US-09-320-424-13	Sequence 13, Appli
15	988	66.8	256	3	US-09-825-563-13	Sequence 13, Appli
16	930	62.9	177	3	US-09-105-343A-7	Sequence 7, Appli
17	930	62.9	291	1	US-08-670-354-6	Sequence 6, Appli
18	930	62.9	291	3	US-09-320-424-6	Sequence 6, Appli
19	930	62.9	291	4	US-09-825-563-6	Sequence 6, Appli
20	930	62.9	291	5	PCT-US96-10895-6	Sequence 6, Appli
21	850	57.5	161	4	US-09-565-423-7	Sequence 7, Appli
22	654	44.2	183	3	US-09-105-343A-8	Sequence 8, Appli
23	482	32.6	101	1	US-08-670-354-4	Sequence 4, Appli
24	482	32.6	101	3	US-09-320-424-4	Sequence 4, Appli
25	482	32.6	101	4	US-09-825-563-4	Sequence 4, Appli
26	482	32.6	101	5	PCT-US96-10895-4	Sequence 4, Appli
27	446	30.2	85	4	US-09-632-287A-12	Sequence 12, Appli

28	258.5	17.5	294	3	US-08-996-139-11	Sequence 11, Appli
29	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appli
30	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appli
31	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appli
32	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appli
33	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appli
34	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appli
35	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appli
36	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appli
37	258.5	17.5	316	2	US-08-842-842-7	Sequence 7, Appli
38	258.5	17.5	316	3	US-08-989-362-2	Sequence 2, Appli
39	258.5	17.5	316	4	US-09-052-521C-2	Sequence 2, Appli
40	258.5	17.5	316	4	US-09-671-658A-2	Sequence 2, Appli
41	258.5	17.5	316	4	US-09-396-937-4	Sequence 6, Appli
42	258.5	17.5	316	4	US-09-396-937-6	Sequence 6, Appli
43	251.5	17.0	317	3	US-08-996-139-13	Sequence 13, Appli
44	251.5	17.0	317	3	US-08-995-659-13	Sequence 13, Appli
45	251.5	17.0	317	3	US-09-215-649A-13	Sequence 13, Appli

ALIGNMENTS

USA

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-670-354-2
Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MAMMEVQGGPSLGGTCTVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTCTVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
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61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
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121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
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Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Method 2

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLGGTCTVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
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61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
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181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-780-496-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLGGTCTVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKQRLQVLVKMILRTSEETISTVQEKQONISPLVREERGPO 120
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181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA

Method 2

ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DDSYWDPNDEESMNSPCWQVKQQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
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DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVTHEKG 180
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DB 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 5

US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368

12811 Porembski

; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-320-424-2

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DDSYWDPNDEESMNSPCWQVKQQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRNGELVTHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 6

US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUENH, ALEMSSEGD
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

modified by [signature]

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCTVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCTVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
DB 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
QY 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYSTYDPDILMKSARNSCWSKDAEYGLY 240
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DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281

under seed

RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMODKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMODKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
DB 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120

QY 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYSTYDPDILMKSARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYSTYDPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281

Ab

RESULT 8
US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMODKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMODKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
DB 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
QY 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYSTYDPDILMKSARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYSTYDPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281

RESULT 9
US-10-039-785-66
; Sequence 66, Application US/10039785

mutated

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; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66
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Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMWQYIYKTSYDPDILMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMWQYIYKTSYDPDILMKSARNSCWSDAEYGLY 240
QY 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 10
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2
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Query Match      100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMWQYIYKTSYDPDILMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMWQYIYKTSYDPDILMKSARNSCWSDAEYGLY 240
QY 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 11
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
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; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-072-993C-3

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Query Match	99.4%	Score 1469;	DB 4;	length 279;
Best Local Similarity	100.0%	Pred. No. 2.5e-148;		
Matches 279;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 3 MMEVQGGPSLGQTCVLIVIFTVLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKEDD 62
 |||||
 Db 1 MMEVQGGPSLGQTCVLIVIFTVLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKEDD 60

	QY	63 SYMDENDEESMNSPCWQVWKQLRÖLVKRMILRTSEETISTVØEKQONISPLVBEGPÖRV 122
	Db	61 SYMDPENDESMSNPCWQVKWLRLÖLVKRMILRTSEETISTVØEKQONISPLVBEGPÖRV 120

[illegible]

QY	183	YIYSQTFRFQEIKENTKNDKOMQYIYKYTSYPDPILMLKSARNSCWSKAEGLYSI	242
Db	181	YIYSQTFRFQEIKENTKNDKOMQYIYKYTSYPDPILMLKSARNSCWSKAEGLYSI	240

QY 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGALVIG 281
 Db 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGALVIG 279

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424

```

; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
;
; LENGTH: 253
; TYPE: PR1
; ORGANISM: synthetic fusion
US-09-320-424-11

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Query Match	66.8%;	Score 988;	DB 3;	Length 253;
Best Local Similarity	78.9%;	Pred. NO. 4.3e-97;		
Matches 194;	Conservative 15;	Mismatches 13;	Indels 24;	Gaps 2;

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39 TNELKQWQDKYSKSGIACFLKEDDSYMDENDESMNSPCWQVK--WQLRQLYVKMIILRT 95
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29 SDRWKQIEDKI-----EELLSKIYHIENEIARIKILGERTRST 67

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QY	96	SEETISTVQEKQOONISPLVREGRFQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE	155
Db	68	SEETISTVQEKQOONISPLVREGRFQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE	127
QY	156	SSRSQHSFLSNLHLRNGEFLYIHEKGFYYIYSQTFRFQOEIKENTKNDKQWQYIYKYTS	215
Db	128	SSRSQHSFLSNLHLRNGEFLYIHEKGFYYIYSQTFRFQOEIKENTKNDKQWQYIYKYTS	187
QY	216	YPDPILIMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF	275
Db	188	YPDPILIMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF	247
QY	276	GAFLVG 281	
Db	248	GAFLVG 253	

[illegible]

QY 216 YPDPILIMKSARNSCWSKDAEYGLSYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFF 275
 |||||
 Db 188 YPDPILIMKSARNSCWSKDAEYGLSYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFF 247

QY	276	GAF	LVG	281
Db	248	GAF	LVG	253

RESULT 13
US-09-825-563-11

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; Sequence 11, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11

```

Query Match	66.8%;	Score 988;	DB 4;	Length 253;
Best Local Similarity	78.9%;	Pred. No. 4.3e-97;		
Matches 194; Conservative	15;	Mismatches 13;	Indels 24;	Gaps 2;

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QY      39  TNELKQWQDKYKSGTACFLKEDDSYWDPNDEESMNSPCWQVK---WQKQLVKMLIRT 95
      :::|::| |::|::| |::|::| |::|::| |::|::| |::|::| |
Db      29  SDRMKQIEDKI-----EELISKYHIENELARIKKLIGERTRST 67
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[illegible]

QY 156 SSRSGHSELSNLHRLNGELVIHEKGFYYIYSQTYPFRFOEIKENTKNDKOMVOIYYKYTS 215
|||
DB 128 SSRSGHSELSNLHRLNGELVIHEKGFYYIYSQTYPFRFOEIKENTKNDKOMVOIYYKYTS 187

QY 216 YPDPILLMKSARNSCWSKDAEYGLYSITYQGIFELKENDRIFVSVTNEHLIDMDHEASFF 275

Db 188 YPDPILLMKSARNSCWSKDAEYGLYSITYQGIFELKENDRIFVSVTNEHLIDMDHEASFF 247

QY	276	GAFLVG	281
Db	248	GAFLVG	253

RESULT 14

US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-13

Query Match 66.8%; Score 988; DB 3; Length 256;
Best Local Similarity 78.9%; Pred. No. 4.4e-97;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVK---WQLRQLVRKMIIRT 95
Db 32 SDRMKQIEDKI-----EELISKIYHIENEIARIKKLIGERTRST 70
QY 96 SEETISTVQEKQONISPLVRRERGPQVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 155
Db 71 SEETISTVQEKQONISPLVRRERGPQVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 130
QY 156 SSRSGHSFLSNLHLRNGELVTHEKGFYYIYSQTYFRFQEI KENTKNDKQMWQYIYKYTS 215
Db 131 SSRSGHSFLSNLHLRNGELVTHEKGFYYIYSQTYFRFQEI KENTKNDKQMWQYIYKYTS 190
QY 216 YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 275
Db 191 YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 250
QY 276 GAFLVG 281
Db 251 GAFLVG 256

RESULT 15

US-09-825-563-13
; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; EARLIER APPLICATION NUMBER: 09/320,424
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25

; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-13

Query Match 66.8%; Score 988; DB 4; Length 256;
Best Local Similarity 78.9%; Pred. No. 4.4e-97;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVK---WQLRQLVRKMIIRT 95
Db 32 SDRMKQIEDKI-----EELISKIYHIENEIARIKKLIGERTRST 70
QY 96 SEETISTVQEKQONISPLVRRERGPQVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 155
Db 71 SEETISTVQEKQONISPLVRRERGPQVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 130
QY 156 SSRSGHSFLSNLHLRNGELVTHEKGFYYIYSQTYFRFQEI KENTKNDKQMWQYIYKYTS 215
Db 131 SSRSGHSFLSNLHLRNGELVTHEKGFYYIYSQTYFRFQEI KENTKNDKQMWQYIYKYTS 190
QY 216 YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 275
Db 191 YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 250
QY 276 GAFLVG 281
Db 251 GAFLVG 256

Search completed: September 5, 2004, 09:27:04
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:23:01 ; Search time 25 Seconds

(without alignments)
1081.193 Million cell updates/sec

Title: US-10-662-431-2

Perfect score: 1478

Sequence: 1 MAMMEVGGPSLGGTCVLIV.....NEHLIDMDHEASFFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	189.5	12.8	279	2	A53062	Fas ligand - mouse
2	186	12.6	281	2	I38707	Fas ligand - human
3	177.5	12.0	278	2	A49266	Fas ligand - rat
4	164	11.1	261	2	S53090	CD40 ligand - bovi
5	147.5	10.0	261	2	I53476	CD40 ligand - huma
6	141	9.5	234	1	A25451	tumor necrosis fac
7	141	9.5	260	2	S21738	CD40 ligand - mous
8	134.5	9.1	204	1	S17289	tumor necrosis fac
9	133	9.0	232	1	S12606	tumor necrosis fac
10	131.5	8.9	233	1	S22052	tumor necrosis fac
11	131	8.9	234	1	JQ1344	tumor necrosis fac
12	130.5	8.8	233	1	S24642	tumor necrosis fac
13	129.5	8.8	235	2	I54490	tumor necrosis fac
14	127.5	8.6	204	1	S24641	lymphotoxin - bovi
15	125.5	8.5	233	1	QWHUN	tumor necrosis fac
16	123.5	8.4	235	2	QWMSN	tumor necrosis fac
17	123.5	8.4	235	2	JU0029	tumor necrosis fac
18	122	8.3	205	1	QWHUX	lymphotoxin alpha
19	121	8.2	234	1	JH0529	tumor necrosis fac
20	115.5	7.8	193	2	S06192	tumor necrosis fac
21	114	7.7	202	1	B27303	tumor necrosis fac
22	113.5	7.7	185	2	S52715	tumor necrosis fac
23	113.5	7.7	306	2	I49139	lymphotoxin-beta
24	112.5	7.6	638	1	QOBY2M	mRNA maturase b14
25	111.5	7.5	202	1	JN0869	tumor necrosis fac
26	109	7.4	652	2	I48083	amphotropic murine
27	107	7.2	197	1	JH0309	tumor necrosis fac
28	102	6.9	244	2	A46066	lymphotoxin beta -
29	100	6.8	865	2	AB1658	probable membrane

30	99.5	6.7	233	2	S11688	tumor necrosis fac
31	97.5	6.6	448	2	F95122	protein kinase, pr
32	95	6.4	345	2	T14707	DNA ligase homolog
33	95	6.4	365	2	T15010	hypothetical prote
34	95	6.4	455	2	G95104	hypothetical prote
35	94.5	6.4	4981	2	T18489	hypothetical prote
36	94	6.4	1465	2	T23056	cytomodomain helic
37	92.5	6.3	833	1	A31593	heat shock transcr
38	92.5	6.3	1538	2	T29095	cardiac muscle fac
39	91	6.2	1176	2	JN0583	myosin-light-chain
40	90.5	6.1	502	2	A53444	activin receptor-1
41	90.5	6.1	502	2	JC2491	serine/threonine k
42	90.5	6.1	1284	2	T40578	hypothetical prote
43	90	6.1	907	2	E96636	hypothetical prote
44	89.5	6.1	313	2	T03031	NBS-LRR type resis
45	89	6.0	328	2	B59296	alpha-N-arabino fur

ALIGNMENTS

RESULT 1

A53062

Fas ligand - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C/Accession: A53062

R/Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nage

Cell 76, 969-976, 1994

A/Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in t

A/Reference number: A53062; MUID:94185175; PMID:7511063

A/Accession: A53062

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-279 <TAK>

A/Cross-references: GB:U06948; NID:9473564; PIDN:AAA17800.1; PID:9473565

Query Match

Best Local Similarity 12.8%; Score 189.5; DB 2; Length 279;

Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY	83	QLRQLVRKMLRTSEETISTVQEKQONISPLVREGRQVAAHITGTRGRSNTLSPPNSK 142
DB	111	ELREFTNQSL-----KVSSFEEKQIANPSTPSEKKEPRSV-AHLTG-----NPHSR 154
QY	143	NEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIYSQTYFRFQELKENTKN 202
DB	155	SIFL-----EWEDT-YGTALISGVKKYKGGVINETGLYFVYSKVYFRGQ-----SCN 201
QY	203	DKQMVQYIV-KYTSYDPDPIILMK SAR-NSCWSKDAEYGLYSIYGGIFELKENDRI FVSV 260
DB	202	NQPLNHKVMYRNKYPEDLVLMEEKRLNYCT--GQIWAHSSYLGAVFNLT SADHLIYVNI 259
QY	261	TNEHLIDMDHEASFFGA F 278
DB	260	SQLSLINFEESEKTFEGLY 277

RESULT 2

I38707

Fas ligand - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: I38707; J02340; S57565; I38554

R/Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A/Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A/Reference number: I38707; MUID:95127560; PMID:7826947

A/Accession: I38707

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-281 <RES>

A/Cross-references: EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: J02340; MUID:95071350; PMID:7980502
A;Accession: J02340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
R;Schatzlein, C.E.
Submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
A;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
Best Local Similarity 22.1%; Pred. No. 3.1e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVGGPSLQTCVLLVIFTVLLQSLCVAV--TVVYFTNELKQMODKYSKSGIACFLKE 60
Db 71 LKKRGNHSTG-LCLLMFMFVVALVGLGFMFQLFHLQKELAELESTSQMHTASSLEK 129
QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 130 QIGHPSPPPE-----KKELRKV----- 146
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 147 --AHLT--GKSNRSMP-----LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
QY 181 FYYIYSQTYFRFQEIETKENTKNDKQWQYIY-KYTSYPPDILMKSAARNS-----CWSK 233
Db 188 LYFVYSKVYFRGQ-----SCNNLPLSHKVMRNSKYPQDLVMEGRKMSYCTTGQMMAR 241
QY 234 DAHYGLYSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Db 242 -----SSYLGAVFNLTSADHLVYNVSELSLVNFEESQTFFGLY 279

RESULT 3
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.6e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVQEKQONISPLVRERGPQVAHAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158
Db 121 VSSFEEKQIANPSTPSETKKRSV-AHLTGNPRSRISPL-----EWEDT- 162
QY 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEIETKENTKNDKQWQYIY-KYTSYP 217
Db 163 YGTALLISGVKYYKKGGLVINEAGLYFVYSKVYFRGQ-----SCNSQPLSHKVMRNFKYP 216
QY 218 DPILMKSAAR-NSCWSKDAEYGLYSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
Db 217 GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLVYNISQLSLINFEESSKTFEG 274
QY 277 AF 278
Db 275 LY 276

RESULT 4
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
Submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA8363.1; PID:g732570

Query Match 11.1%; Score 164; DB 2; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.1e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VGGPSLQTCVLLVIFTVLL-QSLCVAVTVVYFTNELKQMODKYSKSGIACFLKEDDS 63
Db 13 VATGPVSMK-IFMYLLITVFLITQMGSLFAVYLLHRLDKIEDERNLHEDFVEMK--T 68
QY 64 YWDPNDESMNS--PCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 121
Db 69 IQRCNKGEGLSLINCEIRSRFEDLV-KDIMONKE-----VKKEKNFEMHKGQDEPQ- 121
QY 122 VAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178
Db 122 IAAHV-----ISEASSKTTSVL----QW--APKGYTTLSSNLTLENKQLAVKR 165
QY 179 KGFYIYSQTYFRFQEIETKENTKNDKQWQYIYKYTSYPPDILMKSAARNSCWSKDAEY 238
Db 166 QGFYIYITQVTFCSNRE---TLSQAPFIASLCLKSPSGSERILLRAANTHSSSKPC--G 219

QY 239 LYSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
Db 220 QQSIIHLGVFELQSGASVFNVTDPDSQVSHGTGTFSG 257

RESULT 5
CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; J EMO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for

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A:Reference number: S28017; MUID:93049181; PMID:1385114
A:Accession: S28017
A:Molecule type: mRNA
A:Residues: 1-261 <HOL>
A:Cross-references: EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484
R:Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
A:Reference number: JH0793; MUID:93094757; PMID:1281209
A:Accession: JH0793
A:Molecule type: mRNA
A:Residues: 1-261 <SPR>
A:Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
A:Experimental source: peripheral blood T-cell
R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Krocze, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A:Reference number: S26694; MUID:93076854; PMID:1280226
A:Accession: S26694
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A:Accession: S28852; MUID:93138085; PMID:7678552
A:Accession: S28852
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C:Genetics:
A:Gene: GDB:CD40LG; HIGM1; IMD3
A:Cross-references: GDB:120632; OMIM:308230
A:Map position: Xq26-Xq26
C:Keywords: glycoprotein; transmembrane protein
F:13-44/Domain: transmembrane #status predicted <TMM>
F:45-261/Domain: extracellular #status predicted <EXT>
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.0%; Score 147.5; DB 2; Length 261;
Best local Similarity 23.7%; Pred. No. 5.2e-05;
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;

QY 17 VLIVIFTVL--QSLCAVTVYVFTNELQMQDKYSKSGIACFLKEDDSYWP-----ND 69
: : : | | | : : : | : : : : : : : : : : : : : : : : : :
Db 23 IFMYLITVFLITQMIGSALFAVYLLHRRLDKIEDERN-----LHEDVFEMKTIQRCNTG 75
: : : | | | : : : | : : : : : : : : : : : : : : : : : :
QY 70 EESMN-SPCWQYKQLRLVRKMLRTSEFTISTVQEKQNTISPLVBERGPORVAAHITG 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 ERLSLINCEELKSQFEGFVKDML-NKEET-----KKENSFEWQKGDQNPQ-IAAHV-- 126
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSN--LHRLNG-ELVIHEKGFFYYTY 185
: : : | : : : | : : : : : : : : : : : : : : : : : :
Db 127 -----ISEASSKITTSVL-----QW--AEKGYTMSNNLVTLENGKQLTVKRQGLYYTY 172
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 SQTYFRFOEIKENT-----KNDKQMVQYIYKYTSTYDPDILMKARSNSCWSKDAEY 237
: : | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 AQVTFCSNREASSQAPFIASLCLKSPGRFR-----ILLRAANTHSSAKPC-- 218
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 GLYSITYGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
| : : | : : | : : : : : : : : : : : : : : : : : :
Db 219 GQGSIHGLGVFELQPGASVFVNYTDPSSQVSHGTGFTSFG 257
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
J:Accession: A25454; A25451; J50727

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R.Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.,
DNA 5, 149-156, 1986
A>Title: Molecular cloning and expression in *Escherichia coli* of the cDNA coding for rab
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R.Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A>Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserted between residues 6
R.Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- α
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: J50727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62,'Q',63-234 <SHA>
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membr
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

```

Query Match          9.5%; Score 141; DB 1; Length 234;
Best Local Similarity 22.4%; Pred. No. 0.00016;
Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

QY      8 GGP||SLG||Q||TCV||LIV||IF||TVLL||QSL||CAV||TVY||FTNEL||KQ||MQ||KY||SKSG||IA||CF||LKED||DSY||WDP 67
      22 GGP||Q||SK||RC||LC||LS||FS||FL||---VAG||AT||TLF||-----CL||L||--H||FR||VIG||P 58
QY      68 NDE||SM||NS||PC||WQ||YK||MO||LRO||LVR||KMI||-LRT||SE||ET||IST||VO||EK||Q||ON||IS||PL||VR||ERG||PQ||VA||HI 126
      59 QEE||BS||PNN||-----LH||LV||NP||VA||Q||MT||LR||SA||SRAL||SD||-----K||PL||-----A||HV 94
QY      127 TGT||GR||SR||NT||LS||PN||SK||NE||KAL||GR||KIN||SW||ESS||RS||GH||S||PL||SN||LH||RG||EL||VI||HE||KFY||YI||YS 186
      95 VA||-----NP||Q||EG||Q||L||-----Q||WL||S||Q||RA||NAL||L||ANG||M||KL||T||DN||Q||LV||PAD||GL||Y||LI||YS 138
QY      187 Q||TY||FR||Q||OE||IK||ENT||KND||KQ||MV||OY||IY||KY||-TSY||PD||PI||LL||MS||AR||NS||CWS||KDA||EY||G-----LY 240
      139 Q||VL||FS||GQ||-----GCR||SY||VL||LT||HT||VS||RF||AV||SY||PN||KYN||L||LSA||IK||SP||CH||RE||TP||EEA||EP||MA||YE 193
QY      241 SIY||Q||G||IF||EL||KEND||RIF||VS||VT||NE||HL||ID||MD||HEA||S-FFG 276
      194 P||Y||LG||V||F||Q||LE||KGR||LS||TE||VN||O||PEY||LD||LA||ESG||QY||YF||G 230

RESULT 7
CD40 ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C:Accession: S21738
R:Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.N.; Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A:Title: Molecular and biological characterization of a murine ligand for CD40.
A:Reference number: S21738, MUID:92244364, EMID:1374165
A:Accession: S21738
A:Molecule type: mRNA

```


Db 182 EGAEAKPWEPIYLGGVFQLEKDDRLSAEINLPDYIDFAESGQVYFG 228

RESULT 10

S22052

tumor necrosis factor alpha precursor - baboon

C/Species: Papio sp. (baboon)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: S22052

R:Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A/Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A/Reference number: S22052

A/Accession: S22052

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-233 <SAN>

A/Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C/Genetics:

A;Introns: 62/3; 78/1; 94/1

C/Superfamily: tumor necrosis factor

C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131.5; DB 1; Length 233;

Best Local Similarity 19.2%; Pred. No. 0.001;

Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;

QY 2 AMMEVQGPGSLGQTCVLIVFTVLQSLCVAVTYVFTNELKQMÖDKYKSGIACFLKED 61

Db 16 ALPKKTGGPQGSRRCLFLSLFSLIVAGATTLCFLHFGVIGPQREEFPK----- 65

QY 62 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQÖNISPLVREGRGPÖR 121

Db 66 ---DP---SLISPLAQÖ-----VRSSSRTPS-----DK 87

QY 122 VAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKF 181

Db 88 PVAHVVA-----NPQAEQÖL--QWLNRRANALLANGVELRDNQLVVPSSEGL 131

QY 182 YTIYSQTYFRFQÖEIKENTKNDKQWQYIYKYT-----SYDPILMK SARNSGMSK-- 233

Db 132 YLIYSQVLFKGQ-----GCPSTHVLTLTHTISRLAVSYQTKVNLLSAIKSPCQÖRÖTP 182

QY 234 ---DAEYGLYSIYQGIPELKENDRIFVSVTNEHLIDMDHEAS-FFG 276

Db 183 EGAEAKPWEPIYLGGVFQLEKDDRLSAEINLPDYIDFAESGQVYFG 229

RESULT 11

QÖ1344

tumor necrosis factor alpha precursor - horse

N/Alternate names: cachectin; TNF alpha

C/Species: Equus caballus (domestic horse)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: QÖ1344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A/Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis

A/Reference number: QÖ1344; MUID:92084125; PMID:1748301

A/Accession: QÖ1344

A/Molecule type: DNA

A/Residues: 1-234 <STUX>

A/Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C/Comment: This protein is an important proximal mediator of endotoxemia.

C/Genetics:

A;Gene: TNF-alpha

A;Introns: 62/3; 79/1; 95/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb

F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;

Best Local Similarity 20.8%; Pred. No. 0.0011;

Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

QY 8 GGPSTLGTQTCVLIVFTVLQSLCVAVTYVFTNELKQMÖDKYKSGIACFL-----K 59

Db 22 GGPGSRRCLCLSLFSFLL---VAGATTLF-----CLLHFGVIGPQÖR 60

QY 60 EDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQÖNISPLVREGRP 119

Db 61 EEQÖL---PNAFQÖSIN-PLAQÖ-----LRSSSRTPS----- 86

QY 120 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEK 179

Db 87 DKPVAHVVA-----NPQAEQÖL--QWLSGRANALLANGVKLTNDQLVVPLD 130

QY 180 GFYIYSQTYFRFQÖEIKENTKNDKQWQYIYKYT-----SYDPILMK SARNSGMSK 233

Db 131 GLYLIYSQVLFKGQ-----GCPSTHVLTLTHTISRLAVSYPSKVNLLSAIKSPCHTE 181

QY 234 DAEYG-----LYSIYQGIPELKENDRIFVSVTNEHLIDMDHEAS-FFG 276

Db 182 SPEQAEAKPWEPIYLGGVFQLEKDDRLSAEINQPNYIDFAESGQVYFG 230

RESULT 12

S24642

tumor necrosis factor alpha precursor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A/Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tun

A/Reference number: I46046; MUID:94083525; PMID:8260599

A/Accession: I46047

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-233 <CL2>

A/Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C/Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C/Superfamily: tumor necrosis factor

C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 8.8%; Score 130.5; DB 1; Length 233;

Best Local Similarity 20.3%; Pred. No. 0.0013;

Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

QY 3 MMEVQGPGSLGQTCVLIVFTVLQSLCVAVTYVFTNELKQMÖDKYKSGIACFL----- 58

Db 17 LSEKAGGPGSRRCLCLSLFSFLL---VAGATTLF-----CLLHFGV 55

QY 59 ---KEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQÖNISPLVR 115

Db 56 IGPQRESPGÖP---SINSPLYQÖT-----LRSSSQÖSS----- 85

QY 116 ERGPÖRYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175

Db 86 ---NKPVAHVVA-----DINSPQÖLR-----WWDSYANALMANGVKLEDNQÖLV 125

QY 176 IHEKGFYIYSQTYFRFQÖEIKENTKNDKQWQYIYK--YTSYDPILMK SARNSC--- 230

Db 126 VPADGHYLIYSQVLFRGQ-----GCPSTPLFLTHTISRLAVSYQTKVNLLSAIKSPCHRE 180

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:20:06 ; Search time 62 Seconds

(without alignments)
1430.010 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVGGPSLGGTCVLIV.....NEHLIDMDHEASFGALVIG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	963	65.2	287	11 Q8K3G0	Q8K3G0 rattus norv
2	809.5	54.8	304	13 Q7T1F2	Q7T1F2 gallus gall
3	334.5	22.6	317	13 Q7ZYX9	Q7ZYX9 brachydanio
4	307.5	20.8	287	13 Q90WT9	Q90WT9 gallus gall
5	305.5	20.7	214	13 Q9DDZ5	Q9DDZ5 brachydanio
6	184.5	12.5	279	11 Q7TMV9	Q7TMV9 mus musculu
7	180	12.2	252	11 Q8K3Y8	Q8K3Y8 mus musculu
8	178.5	12.1	280	6 Q861W5	Q861W5 mus silve
9	175.5	11.9	169	11 Q9WV90	Q9WV90 marmota mon
10	175	11.8	252	11 Q80YZ0	Q80YZ0 mus musculu
11	173	11.7	252	11 Q8K3Y7	Q8K3Y7 rattus norv
12	166	11.2	251	4 Q8NFE9	Q8NFE9 homo sapien
13	157	10.6	154	6 Q8MJ19	Q8MJ19 macaca mula
14	153.5	10.4	227	13 Q7T2Q3	Q7T2Q3 cyprinus ca
15	144.5	9.8	216	11 Q70332	Q70332 mesocricetu
16	141	9.5	231	13 Q8AW02	Q8AW02 cyprinus ca

17	137.5	9.3	232	11 Q80XA4	Q80XA4 peromyscus
18	135	9.1	156	11 Q91ZL4	Q91ZL4 sigmodon hi
19	135	9.1	215	6 Q9BEE8	Q9bee8 erinaceus e
20	135	9.1	217	11 Q9ERG6	Q9erg6 peromyscus
21	130.5	8.8	222	13 Q7T1T4	Q7T1u4 pagrus majo
22	130.5	8.8	225	13 Q91B41	Q91b41 paralichthy
23	130.5	8.8	225	13 Q91B42	Q91b42 paralichthy
24	128	8.7	230	13 Q8UG37	Q8jg37 ictalurus p
25	127	8.6	253	13 Q7T194	Q7T194 acanthopagr
26	126.5	8.6	215	11 Q99ND1	Q99nd1 tamiasciuru
27	124	8.4	216	6 Q9BEC4	Q9bec4 talpa europ
28	123.5	8.4	216	6 Q9BEC9	Q9bec9 ochotona pr
29	122	8.3	205	4 Q8N4C3	Q8n4c3 homo sapien
30	121.5	8.2	246	13 Q91976	Q91976 oncorhynch
31	121.5	8.2	246	13 Q91970	Q91970 oncorhynch
32	120	8.1	237	13 Q8AWC9	Q8awc9 cyprinus ca
33	119	8.1	202	11 Q80WE7	Q80we7 peromyscus
34	116.5	7.9	217	6 Q9BEG0	Q9beg0 cyclopes di
35	116.5	7.9	217	6 Q9BER4	Q9bef4 cabassous u
36	115.5	7.8	149	6 Q97543	Q97543 aotus nancy
37	113.5	7.7	255	13 Q91810	Q91810 salvelinus
38	113.5	7.7	255	13 Q9DEP9	Q9dep9 oncorhynch
39	112.5	7.6	217	6 Q9BEG1	Q9beg1 bradypus tr
40	112.5	7.6	638	8 Q9Z2W6	Q9z2w6 saccharomyc
41	110	7.4	93	6 Q9TJ2	Q9tj2 bos taurus
42	109.5	7.4	149	6 Q97538	Q97538 aotus vocif
43	109.5	7.4	149	6 Q9TTG8	Q9ttg8 aotus nigri
44	109	7.4	288	13 Q8JHJ4	Q8jhj4 gallus gall
45	109	7.4	652	11 Q60421	Q60421 cricetus

ALIGNMENTS

RESULT 1
Q8K3G0 PRELIMINARY; PRT; 287 AA.
ID Q8K3G0
AC Q8K3G0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA;
RA Mueller A.M., Giegerich G.;
RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY115578; AAM49797.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 11; Length 287;
Best Local Similarity 67.7%; Pred. No. 2.7e-72;
Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;
QY 9 GPSLGG---TCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKEDDSY 64
Db 9 GPSFSQHFMTVICIVLQVLQALIVAVTYMYFNNEVKQLQDNYSKIGIACFSKEDGDF 68

QY 65 WDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVREGRQVAA 124
DB 69 WDSDEGIINRPFCLQVQRQYQYLIIEVTLRTFEKTISTVPEKQOLSTPPLPRGRPRQVAA 128
QY 125 HITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHEKGFYI 184
DB 129 HITGITRRSNMLALIPISKDGKTLGQKLETWESSRGRGHSFLNHVHLRNGELVIOEEGLYI 188
QY 185 YSQTYFRFQE--EIKENTKND----KQWQYIYKYTSYPDPILMKSARNSCWSKDAEY 238
DB 189 YSQTYRFRKEAKEASKTVSKDGRIKQWQYIYKYTSYPDPILMKSARNSCWSREAEY 248
QY 239 LYSITYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 277
DB 249 LYSITYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 287

RESULT 2
Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC Q7T1F2;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN TRAIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
RT "Identification and Characterization of Chicken TNF-Superfamily
RT ligand 8 (CD30 ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
RT Inducing ligand TRAIL).";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114678; BAC79267.1; -
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.8%; Score 809.5; DB 13; Length 304;
Best Local Similarity 55.4%; Pred. No. 1.9e-59;
Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;

QY 8 GGPSLGGTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKEDDSYWP 67
DB 5 GGSPAHTCGAVLVAVLLQSVCAVTYIYFTNELKQMDTYSRSGIACLTGELGLIQ 64
QY 68 N-----DEESMNSPCWQVKQLRQLVKMLRTSEETISTVQ-EKQONISPLVREGRPQ- 120
DB 65 NLDVESKDRVADPCMQVKMHLGKLKKMSRLQENMSAINGDRTQALSR--RDEPPQG 122
QY 121 ---RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTH 177
DB 123 PTLRIAAHLTGSSKRSSA-SPHNYLSYRGIGHKIHMESSRGRGHSFLYNVELMNGELVVP 181
QY 178 EKGFFYYISQTYFRFQEE-----IKENTKNDKQWQYIYKYTSYPDPILMKSARNSCW 231
DB 182 QTGFFYYISQTYFRFRENEDSDGLERIKNPQQLVQYIYKLTNYPDPILMKSARTSCW 241
QY 232 SKDAEYGLYSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
DB 242 SKAEYGLYSVYQGIVFLKREDRIFVSVSNSDIVMDKEASFFGAFMI 290

RESULT 3
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9;
DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Similar to tumor necrosis factor (ligand) superfamily, member 10.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AAH44336.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR Prodom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PSS0049; TNF_2; 1.
DR PROSITE; PSS0049; TNF_2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 22.6%; Score 334.5; DB 13; Length 317;
Best Local Similarity 29.2%; Pred. No. 8.7e-20;
Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;

QY 18 LIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACF-----LKEDSYWDPND-EE 71
DB 40 MWIVVVVVLQIASTGLFVYLNMSLSQVKSQGVTEELRCLGLNVLGKDQDI--PEDLAQ 97
QY 72 SMNSPCWQVKQLRQLVKRM-----ILRTSEETISTVQEKQONISPLVREGRPQ 120
DB 98 LFGEPCMKLAEGIKAYISKVTDSTISKOTLHAARTRTHSYNTTSGKEMTV-----MQ 150
QY 121 RVAAHITGTRGRSNT-----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
DB 151 RPSAHLTLSSASDNSRPQSDMHQPPQDLHQSCRHPVHTW-ANKSFGAHLNMTLTNGRLR 209
QY 176 IHEKGFYYISQTYFRF-QEEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKD 234
DB 210 VPQDGRYYLSQYFRYPSPSPSDQSSVSHQLVQCTYKKTSTYLNPIQLKGVGTCWAPD 269
QY 235 AEYGLYSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
DB 270 AEYALHSVYQGIFELRAGDEVFVSVSPIMVYGEDSSSYFGAF 313

RESULT 4
Q90WT9 PRELIMINARY; PRT; 287 AA.
AC Q90WT9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AAL23702.1; -
DR HSSP; O35235; 1IOA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PSS0049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match	20.8%;	Score 307.5;	DB 13;	Length 287;
Best Local Similarity	32.3%;	Pred. No. 1.4e-17;		
Matches	93;	Conservative	46;	Mismatches 110;
			Indels	39;
			Gaps	11;

```

QY 18 LIVIFTVLLQ--SLCVAVTVVYFT-----NELKOM--QDKYSKSGIACFLKEDDSYWD 66
Db 8 LHAFLSELQLLPLCTAPEMAEGTWSQALQGNAPFRPKAQSGSSSELRCLQTLINQOQEG 67
QY 67 PNDEESM-NSPCWQVKMQLRQLVRKMLRTSEETI--STVOEKQO--NISP-LYBERGP 119
Db 68 SNLEELISNOSC---LKLANTIKAYAVTVENVISRSVNVNEAQKSYFNISEGQVATKTL 123
QY 120 QRVAHI-----TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLR 170
Db 124 GKPSAHLIFRPQNPADGSSRRFGNLS-----QSCRHAITRWEDS-TIHSHLQNTYR 175
QY 171 NGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPLMKSAARNSC 230
Db 176 DGRLRVNQAGKYVVSQIYFRYSRDGAGARVSVQVLVQCINMKTISYSQPIILLKGVGTKC 235
QY 231 WSKDAEYGLYSITYQGGIFELKENDRITFVSVTNEHLIDMDHEASFGAF 278
Db 236 WAPAEYGLHALYQGGIFELKAGDELFVSVSSLAIDYSDAASYFGAF 283

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RESULT 5			
ID	Q9DDZ5	PRELIMINARY;	PRT; 214 AA.
AC	Q9DDZ5;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	TRAIL-like protein.		
GN	TNFSF10L.		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifc		
OC	Cyprinidae; Danio.		
OX	NCBI_Taxid=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Bobe J., Goeltz F.W.;		
RT	"Molecular cloning and expression of a TNF receptor and two TNF		
RT	ligands in the fish ovary."		
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).		
DR	EMBL; AF250041; AAG47640.1; -.		
DR	HSSP; P50591; 1D2Q.		
DR	ZF1N; ZDB-GENE-010801-1; tnfsf10l.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR006052; TNF_family.		
DR	InterPro; IPR008983; TNF_like.		
DR	InterPro; IPR003636; TNF_subf.		
DR	Pfam; PF00229; TNF; 1.		
DR	ProDom; PD002012; TNF_subf; 1.		
DR	SMART; SM00207; TNF; 1.		
DR	PROSITE; PS50049; TNF_2; 1.		
QO	SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;		

Query Match 20.7%; Score 305.5; DB 13; Length 214;

Best Local Similarity 37.6%; Pred. No. 1.4e-17;
Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;

QY 120 QVAAHITGTRKSNT-----LSSPNKNEKALGRKINSWESSRSGHSPLNLHLRNCEL 174
 ||::||: | : | ::|::|: |::|: ||
Db 47 QRPSAHTLTSSASDNSRPQSDMHQPQFDLHQSCRHPVHTW-ANKSFGAHLNMTLTNGRL 105

QY 175 VIHEKGFIYYISQTYFRF-QEEIKENTKNDKOMVOIYYKYTSYPDPILMKARSNSCWSK 233
 : : ||:||: ||: : : ||:||: ||: ||: ||: ||:
Db 106 RVPQDGRYYLYSQYFYERYPSPSPSDQSIVSHQLVQCIIYKTSTYLNPQLLKGVGTKWAP 165

QY 234 DAEYGLSYIOGGIFELKENDRIFSVYTNEHLIDMDHEASFEGAF 278
 ||||: |:||||: ||: |::||:: : : : : ||: ||
Db 166 DAELYALHSVQGGLFELLRAGDEVFVSVPSTMVYGEDSSSYFGAF 210

RESULT 6		
Q7TMV9		
ID	Q7TMV9	PRELIMINARY; PRT; 279 AA.
AC	Q7TMV9;	
DT	01-OCT-2003 (TREMBlrel. 25, Created)	
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)	
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)	
DE	Tnfstf6 protein.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [21]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX Strausberg R.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC052866; AAH52866.1; -.
SQ SEQUENCE 279 AA; 31416 MW; C2972E2728FBBB7B CRC64;

Query Match	12.5%;	Score 184.5;	DB 11;	Length 279;
Best Local Similarity	25.3%;	Pred. No. 2.4e-07;		
Matches 50; Conservative	51;	Mismatches 64;	Indels 33;	Gaps 9;

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QY      83 QLBQLVAKMILRTSEETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNK 142
      :||:      :||:      :||:      :||:      :||:      :||:      :||:
Db      111 ELREFINQSL-----KVSSFQKQIANPSTPSEKKEPRSV-AHITG-----NPHSR 154

QY      143 NEKALGRKINSWESSRSGHSPLSNLILRNGELVIHEKGFYIYSQTYFRFOEIKENTKN 202
      :      :||:      :||:      :||:      :||:      :||:      :||:
Db      155 SIPL-----EWEDT-YGTALISGVKYYKKGGVLINETGLYFYVSKVYFRGQ-----SCN 201

QY      203 DKQWVOIY-KYTSYPDPILMKSAF-NSCWSKDAEYGLYSITYQGQIFELKENDRIFAVSF 260

```

Db 202 NOPLNHKYYMNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSHLCGAVENLTSADHLVNT 259
QY 261 TNEHLIDMDHEASFFGAF 278
Db 260 SOLSLINFESKTFEGLY 277

RESULT 7

Q8K3Y8 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE TNF superfamily ligand TllA.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=21909416; PubMed=11911831;
RA Miyone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TllA is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
cell costimulator.";
RL Immunity 16:479-492(2002).
DR EMBL; AF520786; AAM77367.1; -.
DR MGD; MGI:2180140; Tnfsf15.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PSS0049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;

Query Match 12.2%; Score 180; DB 11; Length 252;
Best Local Similarity 32.4%; Pred. No. 5.1e-07;
Matches 69; Conservative 26; Mismatches 80; Indels 38; Gaps 12;

QY 83 QLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSK 142
Db 63 QLRVPKDCMLRAITERSE-PSPOQVSP--PRGKPR-AHLT-----IKKQTPAPHLK 112
QY 143 NE-KALGRKINSWESSRSGHSPLSN-LHLRNGELVTHEKGFYYISQTYFRFQEEI----- 196
Db 113 NQLSAL-----HWEHD-LGMAFTKNGMKYINKSLVIPESGDYFIYSQITFRGTTSVCGDI 166
QY 197 ---KENTKNDKQWQYIYKYTSYDPDPIILMKSAARNSC-----WSKDAEYGLYSIQGGIF 248
Db 167 SRGRPRNKPDSITVVTITKADSYPEPARLLTGSKSVCEISNNW-----FQSLYLGAMF 219
QY 249 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAFIV 280
Db 220 SLEEGDRLMVNVSISLVYTKEDKTFFGAFLI 252

RESULT 8
Q861W5 PRELIMINARY; PRT; 280 AA.
ID Q861W5;
AC Q861W5;

DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fas ligand.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99053606; PubMed=9839871;
RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,
RA Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL Vet. Immunol. Immunopathol. 65:161-172(1998).
DR EMBL; AB009280; BAC76426.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PSS0049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31361 MW; 6AA7E2DE1F1A6B5C CRC64;

Query Match 12.1%; Score 178.5; DB 6; Length 280;
Best Local Similarity 21.2%; Pred. No. 7.7e-07;
Matches 58; Conservative 53; Mismatches 77; Indels 85; Gaps 11;

QY 16 CVLIVFTVLQSLCVAV--TYVYFTNELKOMQDKYSKSGIACFLKEDDSYWDPNDEES 72
Db 81 CLLVMFEMVLVALVGLGMFQLFHLQKELAELEBSTSQKHVAASLEKQIGQLNPSEK- 139
QY 73 MNSPCWQVKQQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQVAAHITGTRGR 132
Db 140 -----REL-----RKVAHLTG----- 150
QY 133 SNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHLRNGELVTHEKGFYYISQTYFRF 192
Db 151 -----KPNRSRSLP-----EWEDT-YGIALVSGVKYKKGGVLINDTGMFYYSKVNFRG 198
QY 193 QEIEIKENTKNDKQWQYIY-KYTSYDPDPIILMK-SARNSC-----WSKDAEYGLYSIQG 245
Db 199 Q-----SCNNQPLNHKYYMNSKYPQDLVLMEGKMMNYCTTGQMWAR-----SSYLIG 245
QY 246 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Db 246 AVENLTSADHLVYVNSLSLVSEFSKTFEGLY 278

RESULT 9
Q9WV90 PRELIMINARY; PRT; 169 AA.
ID Q9WV90;
AC Q9WV90;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.

OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR HSSP; P50591; 1D4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 11.9%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 7.2e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 83 QLRQLVRKMLIRTSEETISTVQEKQONISPLVREKGPQRYAAHITGTRGSNTLSSPNSK 142
AC Q8K3Y7; PRELIMINARY; PRT; 252 AA.
DB 10 ELKESINQ--RNTPEPL-----EKQIGHPSPPSKKALRAAHLT--GKPNSSRSP--- 56

QY 143 NEKALGRKINSWESSRSGHFLSNLHRLNGELVHEKGFYIYSQTYFRFQEEIKENTKN 202
DB 57 -----LEWEDT-YGISLISGVKYQKGGLVINDTGLYFYYSKIYFRGQ-----SCN 100

QY 203 DKQWQYIY-KYTSYDPDILMK-SARNSC-----WSKDAEYGLYSIYGGIFELKENDR 255
DB 101 NQPLSHKVVVKNKSKYPQDLVMEGKMNNYCTTGQWWR-----SSYLGAVENTSNDH 153

QY 256 IFVSVTNEHLIDMD 269
DB 154 LYVNVSESLINFE 167

RESULT 10
Q80YZ0
AC Q80YZ0; PRELIMINARY; PRT; 252 AA.
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE BM20K13.3 (Tumor necrosis factor (ligand) superfamily, member 15).
DE TNFSF15.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sycamore N.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL691468; CAD83021.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27725 MW; A63ABDCC9E969E0F CRC64;

Query Match 11.8%; Score 175; DB 11; Length 252;
Best Local Similarity 31.9%; Pred. No. 1.3e-06;
Matches 68; Conservative 26; Mismatches 81; Indels 38; Gaps 12;

QY 83 QLRQLVRKMLIRTSEETISTVQEKQONISPLVREKGPQRYAAHITGTRGSNTLSSPNSK 142
DB 63 QLRVPGKDCMLRAITEERSE-PSDQVYSP--PRGKPR--AHLT----IKQTPAPHLK 112

QY 143 NE-KALGRKINSWESSRSGHFLSN-LHLRNGELVHEKGFYIYSQTYFRFQEEI----- 196
DB 113 NQLSAL-----HWEHD-LGMALFTKNGMKYINKSLVIPESGDYFIYSQITFRGTSVCGDI 166

QY 197 --KENTKNDQWQYIYKYTSYDPDILMKARNSC-----WSKDAEYGLYSIYGGIF 248
DB 167 SRGRPNKPSDITMTVITKVDSPYEPARLLTGSKSVCEISNNW-----FQSLYLGAIF 219

QY 249 ELKENDRIFVSVTNEHLIDMDHE-ASFECAFLV 280
DB 220 SLEEGDRLMVNVSDISLVDYTKEDKTEFFGAFL 252

RESULT 11
Q8K3Y7
AC Q8K3Y7; PRELIMINARY; PRT; 252 AA.
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE TNF superfamily ligand Tl1A.
GN TNFSF15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "Tl1A is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
cell costimulator.";
RL Immunity 16:479-492(2002).
DR EMBL; AF520787; AAM77368.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789BE6556D46F293 CRC64;

Query Match 11.7%; Score 173; DB 11; Length 252;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head Kidney;
RA Savan R., Sakai M.;
RT "Cloning of tumor necrosis factor 3 alpha in carp."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB112424; BAC77690.1;
SQ SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;

Query Match 10.4%; Score 153.5; DB 13; Length 227;
Best local Similarity 20.1%; Pred. No. 7.2e-05;
Matches 60; Conservative 50; Mismatches 92; Indels 97; Gaps 11;

QY 3 MMEVQGGP-----SLGQTCVLIYFTVLLQSLCVAWTVVYFTNELKQMDKYSK 51
Db 1 MMDLESQELPQEMVSRNRNASSSSKSAVWVCGVLLAVLCAAAAVCFTLNK----- 50
QY 52 SGIAFLKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRSTSEETISTVQEKQNIS 111
Db 51 -----NNQEGGNE-----QRLTLKDN----- 66
QY 112 PLVREGRQVRVAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHLRN 171
Db 67 -LSKENVTSKVAIHLGA-----YEPDVSKNNIDWKONQDGAFAVSGGLKLV 112
QY 172 GELVIHEKGFYIYSQTYFRFQEIENKTKNDKQMVQYIKYTSYPD-----PILMKS 225
Db 113 REILIPNDGIYFYSQVSFHI--SCNDMTEDQEVMHVSHAVFHYSDFFGIYKP--LIRA 168
QY 226 ARNSCW----SKDAEYGLYSTIYQGIFFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 278
Db 169 ARSACVHASNTEDVWYD--TIYGAASFRLRAGDKLCTKTTELLPRVETDNAKTFEGVF 225

RESULT 15

ID 070332 PRELIMINARY; PRT; 216 AA.
AC 070332;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis."
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046215; AAC40100.1; -
DR HSSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADAE3F83F45B533 CRC64;

Query Match 9.8%; Score 144.5; DB 11; Length 216;
Best local Similarity 26.9%; Pred. No. 0.00038;
Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 118 GPQVRVAH---ITGRGRSNTL--SSPNSKNEKALGRKINS-----WESSRSGHSFLS 165
Db 49 GPQREKEFPNPPIIGSMGQTLTLRSSSQNSNDKPVGHVAVANHQVEEQLEMLSHRANALLAN 108
QY 166 NMLRNGELVIHEKGFYIYSQTYFRFQEIENKTKNDKQMVQYIK-----YTSYPD 218
Db 109 GMSLKDNQLVIPADGLVLYVSQVLFRRQ-----GCPSTVLLTHTVSRIVASYED 157
QY 219 PILMKSARNSCWSKDAEYG-----LYSIYQGIFFELKENDRIFVSVTNEHLID 267
Db 158 NVNLLSAIKSPC-PKETPEGEELKWEYEPYILGGVFQLEKGDRLSAEVNLPKYL 211

Search completed: September 5, 2004, 09:26:11
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:19:21 ; Search time 69 Seconds

(without alignments)
1150.664 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVQGQPSLGGTCVLLV.....NEHLIDMDHEASFFGAFVLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	2 AAW19777	Aaw19777 Novel cyt
2	1478	100.0	281	2 AAW27134	Aaw27134 Human Apo
3	1478	100.0	281	2 AAW19787	Aaw19787 Human apo
4	1478	100.0	281	2 AAW76829	Aaw76829 Human TL2
5	1478	100.0	281	2 AAW56760	Aaw56760 Human TRA
6	1478	100.0	281	2 AAW44354	Aaw44354 Human AGP
7	1478	100.0	281	2 AAY01517	Aay01517 Protein a
8	1478	100.0	281	2 AAY27012	Aay27012 Human Apo
9	1478	100.0	281	3 AAY81956	Aay81956 Human Apo
10	1478	100.0	281	3 AAB24038	Aab24038 Human PRO
11	1478	100.0	281	3 AAB08545	Aab08545 Amino aci
12	1478	100.0	281	3 AAB28691	Aab28691 Human AGP
13	1478	100.0	281	4 AAB50977	Aab50977 Human PRO
14	1478	100.0	281	4 AAB67243	Aab67243 Human Apo
15	1478	100.0	281	4 AAE11031	Aae11031 Human TNF
16	1478	100.0	281	4 AAB48350	Aab48350 Human TL2
17	1478	100.0	281	5 ABB08133	Abb08133 Human TRA
18	1478	100.0	281	5 ABG31630	Abg31630 Human TRA
19	1478	100.0	281	5 AAU75062	Aau75062 Human TNF
20	1478	100.0	281	5 AAM51077	Aam51077 Human Apo
21	1478	100.0	281	5 ABP51954	Abp51954 Human Apo
22	1478	100.0	281	5 AAO19095	AAo19095 C neoform
23	1478	100.0	281	5 AAU79593	Aau79593 Human TNF
24	1478	100.0	281	6 ABG73861	Abg73861 Human Apo
25	1478	100.0	281	6 ABU10205	Abu10205 Human Apo

26	1478	100.0	281	6 ABU71443	Abu71443 Human neo
27	1478	100.0	281	6 ABG72738	Abg72738 Human TNF
28	1478	100.0	281	6 AAO29543	Aao29543 Human TRA
29	1478	100.0	281	6 ABU08558	Abu08558 Human TNF
30	1478	100.0	281	6 ABR42313	Abrr42313 Human TRA
31	1478	100.0	281	6 ABG71905	Abg71905 Human TRA
32	1478	100.0	281	6 ABP60546	Abp60546 Human tum
33	1478	100.0	281	6 AAB36258	Aae36258 Human TR4
34	1478	100.0	281	6 AAO31151	Aao31151 Human TNF
35	1478	100.0	281	6 ABO25125	Abo25125 Human TNF
36	1478	100.0	281	7 ADB61471	Adb61471 Native hu
37	1478	100.0	281	7 ADC35202	Adc35202 Human TNF
38	1478	100.0	281	7 ADD14080	Add14080 Human src
39	1478	100.0	281	7 ADD19010	Add19010 Human dis
40	1478	100.0	281	8 ADE76953	Ade76953 Human pro
41	1475	99.8	281	7 ADB61488	Adb61488 Human Apo
42	1473	99.7	281	5 ABG72257	Abg72257 Human tum
43	1473	99.7	281	7 ADB61478	Adb61478 Human Apo
44	1473	99.7	281	7 ADB61477	Adb61477 Human Apo
45	1473	99.7	281	7 ADB61479	Adb61479 Human Apo

ALIGNMENTS

RESULT 1	
AAW19777	standard; protein; 281 AA.
ID	AAW19777
XX	AAW19777;
AC	22-SEP-1997 (first entry)
XX	
DT	Novel cytokine Apo-2 ligand.
XX	
DE	Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.
XX	
KW	Homo sapiens.
XX	
OS	
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..281
FT	/note= "Claim 4"
FT	1..14
FT	/label= Cytoplasmic_region
FT	15..281
FT	/note= "Claim 3"
FT	15..40
FT	/label= Transmembrane_region
FT	41..281
FT	/note= "Claim 2"
FT	41..281
FT	/label= Extracellular_region
FT	109
FT	/label= Glycosylation
FT	/note= "putative N-linked glycosylation site"
FT	114..281
FT	/note= "Claim 1"
XX	
PN	WO9725428-A1.
XX	
PD	17-JUL-1997.
XX	
PF	08-JAN-1997; 97WO-US000272.
XX	
PR	09-JAN-1996; 96US-00584031.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX	
DR	WPI; 1997-372867/34.
DR	N-PSDB; AAT72796.
XX	

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT apoptosis for the treatment of breast and colon cancer.

PS Claim 4; Fig 1a; 72pp; English.

XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
CC cell apoptosis. It is believed to be a member of the tumour necrosis
CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
CC clone (AA72796) isolated from a human placental cDNA library. Apo-2
CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
CC acid. They can be used to induce apoptosis in mammals and to treat
CC pathological conditions such as cancer (esp. breast or colon cancer) or
CC to raise antibodies useful in diagnostic assays

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLIGQTCVLIVIFVTLLQSLCVAVTYVYFTNELKQMMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLIGQTCVLIVIFVTLLQSLCVAVTYVYFTNELKQMMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHSFLSNLHRLNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQOEIKENTKNDKQMVQYIYKTSYPPDILMLKSARNSCWSDAEYGLY 240
Db 181 FYYIYSQTYFRFQOEIKENTKNDKQMVQYIYKTSYPPDILMLKSARNSCWSDAEYGLY 240

QY 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
AAW27134
ID AAW27134 standard; protein; 281 AA.

XX AAW27134;
AC XX
DT 02-APR-1998 (first entry)

XX Human Apoptosis inducing molecule-I (AIM-I).

XX Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.

XX Homo sapiens.

XX WO9733899-A1.

XX 18-SEP-1997.

XX 14-MAR-1996; 96WO-US003773.

XX 14-MAR-1996; 96WO-US003773.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM;

XX MPI; 1997-470807/43.

XX N-PSDB; AAT85210.

XX New isolated apoptosis inducing molecule-I - used to develop products for
PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
PT versus host disease or inflammation.

PS Claim 2; Fig 1; 82pp; English.

XX The present sequence represents a human Apoptosis inducing molecule-I
CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
CC superfamily. The products can be used in the diagnosis and treatment of
CC disorders related to under-expression, over-expression or altered
CC expression of AIM-I. AIM-I or agonists can be used for treating
CC autoimmune disorders including systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
CC haematopoiesis in endothelial cell development, to stimulate peripheral
CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
CC osteoporosis, for preventing graft-host rejection, and as anti-
CC inflammatory agents, for treating endotoxemic shock or to prevent
CC activation of HIV

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLIGQTCVLIVIFVTLLQSLCVAVTYVYFTNELKQMMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLIGQTCVLIVIFVTLLQSLCVAVTYVYFTNELKQMMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHSFLSNLHRLNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQOEIKENTKNDKQMVQYIYKTSYPPDILMLKSARNSCWSDAEYGLY 240
Db 181 FYYIYSQTYFRFQOEIKENTKNDKQMVQYIYKTSYPPDILMLKSARNSCWSDAEYGLY 240

QY 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3
AAW19787
ID AAW19787 standard; protein; 281 AA.

XX AAW19787;

XX 24-SEP-1997 (first entry)

XX Human apoptosis inducer cytokine TRAIL.

XX Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..18
FT Domain
FT /label= Cytoplasmic_domain
FT 19..38
FT Domain
FT /label= Transmembrane_domain
FT 39..281


```
FT FT /label= Extracellular_domain
FT FT /note= "contains a receptor-binding region"
FT FT 89..90
FT FT Cleavage-site
FT FT /note= "potential KEX2 protease processing site"
FT FT 109..111
FT FT Modified-site
FT FT /note= "potential N-glycosylation site"
FT FT 149..150
FT FT Cleavage-site
FT FT /note= "potential KEX2 protease processing site"
PN WO9701633-A1.
XX 16-JAN-1997.
XX
XX
XX
XX
XX 25-JUN-1996; 96WO-US010895.
XX
XX
XX 29-JUN-1995; 95US-00496632.
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX
XX PI Wiley SR, Goodwin RG;
XX
XX WPI; 1997-118715/11.
XX DR N-PSDB; AAT72847.
XX
XX
XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
XX PT cells - useful for treating thrombotic microangiopathy, cancer and viral
XX PT infection and for use in assays.
XX
XX PS Claim 10; Page 43-44; 62pp; English.
XX
XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
XX CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
XX CC cells, including cancer cells and virally infected cells. Its amino acid
XX CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
XX CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
XX CC polypeptides) can be expressed in host cells and used in the treatment of
XX CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
XX CC to raise antibodies that may be useful for treating thrombotic
XX CC microangiopathies
XX
XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPIILMK SARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPIILMK SARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
AAW76829
ID AAW76829 standard; protein; 281 AA.
XX
XX AC AAW76829;
```

```
XX XX
XX DT 25-JAN-1999 (first entry)
XX XX
XX DE Human TL2 protein.
XX XX
XX KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;
XX KW inflammation; arthritis; septicemia; autoimmune disease; restenosis;
XX KW transplant rejection; infection; ischemia; brain injury; bone disease;
XX KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;
XX KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
XX KW TL2. tumour necrosis factor-related apoptosis-inducing ligand.
XX
XX OS Homo sapiens.
XX
XX PN EP870827-A2.
XX
XX PD 14-OCT-1998.
XX
XX PF 23-DEC-1997; 97EP-00310562.
XX
XX PR 14-MAR-1997; 97US-0041230P.
XX PR 09-MAY-1997; 97US-00853684.
XX PR 22-AUG-1997; 97US-00916625.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Deen KC, Young PR;
XX
XX DR WPI; 1998-523156/45.
XX DR N-PSDB; AAV63096.
XX
XX
XX PT DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX PT polypeptide, antibody, agonist, antagonist, etc.
XX
XX PS Disclosure; Page 32-33; 34pp; English.
XX
XX CC This sequence represents the human tumour necrosis factor (TNF)-related
XX CC receptor, TL2 (also known as tumour necrosis factor-related apoptosis-
XX CC inducing ligand, TRAIL). This protein is used in a method resulting in
XX CC the isolation of the novel human TNF related receptor, TR6. TR6
XX CC polypeptides and polynucleotides can be used in the treatment of chronic
XX CC and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.
XX CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX CC host disease, infection, stroke, ischemia, acute respiratory disease
XX CC syndrome, restenosis, brain injury, (acquired autoimmune disease
XX CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
XX CC disorders), atherosclerosis and Alzheimers disease
XX
XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPIILMK SARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPIILMK SARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
```

RESULT 5				
AAW56760	ID	AAW56760	standard; protein; 281 AA.	
XX	AC	AAW56760;		
XX	DT	05-AUG-1998	(first entry)	
XX	DE	Human TRAIL polypeptide.		
XX	KM	Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;		
XX	KW	cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.		
OS	OS	Homo sapiens.		
XX	XX			
FT	FT	Key	Location/Qualifiers	
FT	FT	Domain	1..18	
FT	FT	Region	/note= "N-terminal cytoplasmic domain"	
FT	FT	Domain	19..38	
FT	FT		/note= "transmembrane region"	
FT	FT		39..281	
FT	FT		/note= "extracellular domain"	
XX	XX			
PN	PN	US5763223-A.		
XX	XX			
PD	PD	09-JUN-1998.		
XX	XX			
PF	PF	25-JUN-1996;	96US-00670354.	
XX	XX			
PR	PR	29-JUN-1995;	95US-00496632.	
XX	XX	01-NOV-1995;	95US-00548368.	
XX	PA	(IMMV) IMMUNEX CORP.		
XX	PI	Goodwin RG, Wiley SR;		
XX	DR	WPI; 1998-347322/30.		
DR	DR	N-PSDB; AAV29518.		
XX	PT	DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful		
PT	PT	for producing recombinant polypeptides for research and therapy of		
PT	PT	leukaemia, lymphoma, melanoma and viral infections.		
XX	PS	Claim 1; Col 33-36; 28pp; English.		
XX	CC	This represents a human tumour necrosis factor related apoptosis ligand		
CC	CC	(TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce		
CC	CC	apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful		
CC	CC	for producing the recombinant TRAIL polypeptides, which may be useful in		
CC	CC	studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells		
CC	CC	(e.g. to isolate antigens for vaccine development). The polypeptides can		
CC	CC	be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal		
CC	CC	treatment of blood or bone-marrow), or to treat viral infections		
XX	XX			
SQ	SQ	Sequence 281 AA;		
QY	QY	Query Match	100.0%; Score 1478; DB 2; Length 281;	
Db	Db	Best Local Similarity	100.0%; Pred. No. 2.6e-137;	
QY	QY	Matches	281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	Db			
QY	QY	1 MAMMEVQGPGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE	60	
Db	Db	1 MAMMEVQGPGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE	60	
QY	QY	61 DDSYWDPNDEESMNSPCWQVKWQLRQLVVKMILRTSEETISTVQEKQONISPLVREGRPQ	120	
Db	Db	61 DDSYWDPNDEESMNSPCWQVKWQLRQLVVKMILRTSEETISTVQEKQONISPLVREGRPQ	120	
QY	QY	121 RVAAHITGTRGRSNTLISSPNSKNEKALGRKINSWESSRSGHSFLSNLHIRNGELVIHEKG	180	
Db	Db	121 RVAAHITGTRGRSNTLISSPNSKNEKALGRKINSWESSRSGHSFLSNLHIRNGELVIHEKG	180	

QY	QY	181 FYYIYSQTYFRFQEEIKENTKNDKOMVOYIYKXTSYDPDILMKSARNSCWSKDAEYGLY	240	
Db	Db	181 FYYIYSQTYFRFQEEIKENTKNDKOMVOYIYKXTSYDPDILMKSARNSCWSKDAEYGLY	240	
QY	QY	241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG	281	
Db	Db	241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG	281	
RESULT 6				
AAW44354	ID	AAW44354	standard; protein; 281 AA.	
XX	AC	AAW44354;		
XX	DT	28-MAY-1998	(first entry)	
XX	DE	Human AGP-1.		
XX	KW	Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;		
XX	KW	bone resorption; haematopoietic disease.		
OS	OS	Homo sapiens.		
XX	XX			
PN	PN	WO9746686-A2.		
XX	XX			
PD	PD	11-DEC-1997.		
XX	XX			
PF	PF	06-JUN-1997;	97WO-US009895.	
XX	XX			
PR	PR	07-JUN-1996;	96US-00660562.	
XX	XX	(AMGE-) AMGEN INC.		
XX	PI	Johnson MJ, Simonet WS, Danilenko DM;		
XX	DR	WPI; 1998-042194/04.		
DR	DR	N-PSDB; AAV15295.		
XX	PT	Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -		
PT	PT	useful for treating inflammation, bone resorption and haematopoietic		
PT	PT	diseases.		
XX	PS	Claim 7; Page 36-37; 54pp; English.		
XX	CC	The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis		
CC	CC	factor (TNF)-related protein, involved in inflammation, myelopoiesis and		
CC	CC	bone resorption. It has the same nucleic acid and amino acid (aa)		
CC	CC	sequences as the TNF-related apoptosis-induced ligand (TRAIL) described		
CC	CC	in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay		
CC	CC	reagents for detecting AGP-1 expression. Nucleic acid complementary to		
CC	CC	AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are		
CC	CC	used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus		
CC	CC	erythematosus, psoriasis, scleroderma, infection-related inflammation) or		
CC	CC	bone resorption diseases (e.g. osteoporosis, osteomyelitis,		
CC	CC	hypercalcaemia, Paget's disease). AGP-1 can be used to treat		
CC	CC	haematopoietic diseases associated with reduction in the number of bone		
CC	CC	marrow cells, particularly neutrophils and lymphocytes, e.g. where caused		
CC	CC	by disease, injury or exposure to myelosuppressive agents. Host cells,		
CC	CC	transformed with expression vectors containing AGP-1 DNA, are used to		
CC	CC	produce recombinant AGP-1		
XX	XX			
SQ	SQ	Sequence 281 AA;		
QY	QY	Query Match	100.0%; Score 1478; DB 2; Length 281;	
Db	Db	Best Local Similarity	100.0%; Pred. No. 2.6e-137;	
QY	QY	Matches	281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	Db			
QY	QY	1 MAMMEVQGPGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE	60	
Db	Db	1 MAMMEVQGPGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE	60	

QY 61 DDSYWDPNDESMNSPCWQVKQRLRLVRKMLIRTSEETISTVQEKQONISPLVREGRGPQ 120
Db 61 DDSYWDPNDESMNSPCWQVKQRLRLVRKMLIRTSEETISTVQEKQONISPLVREGRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 7
AAAY01517
ID AAAY01517 standard; peptide; 281 AA.
XX
AC AAAY01517;
XX
DT 27-MAY-1999 (first entry)
XX
DE Protein associated with neurodegenerative and autoimmune diseases.
XX
KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX
OS Homo sapiens.
XX
PN FR2766713-A1.
XX
PD 05-FEB-1999.
XX
PF 04-AUG-1997; 97FR-00010176.
XX
PR 04-AUG-1997; 97FR-00010176.
XX
PA (INMR) BIO MERIEUX.
XX
PI Rieger F, Belliveau JF, Perron H;
XX
DR WPI; 1999-156177/14.
XX

PT Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.
XX
XX
PS Claim 2; Page 13; 21pp; French.
XX
XX

CC The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part of the present sequence to produce a
CC diagnostic, prophylactic or therapeutic composition useful in cases of
CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
CC be used in treatment of neurodegenerative disease, lupus erythematosus,
CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
CC nervous system cells, antigenic and specifically recognise the surface
CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex
XX
XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCWQVKQRLRLVRKMLIRTSEETISTVQEKQONISPLVREGRGPQ 120
Db 61 DDSYWDPNDESMNSPCWQVKQRLRLVRKMLIRTSEETISTVQEKQONISPLVREGRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQOEIKENTKNDKQWQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 8
AAAY27012
ID AAAY27012 standard; protein; 281 AA.
XX
AC AAAY27012;
XX
DT 24-SEP-1999 (first entry)
XX
DE Human Apo-2 ligand (Apo-2L) polypeptide.
XX
KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
KW lupus; immune-mediated glomerular nephritis; human.
XX
OS Homo sapiens.
XX
PN WO9936535-A1.
XX
PD 22-JUL-1999.
XX
PF 15-JAN-1999; 99WO-US001039.
XX
PR 15-JAN-1998; 98US-00007886.
XX
PR 15-APR-1998; 98US-00060533.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
XX
XX

DR WPI; 1999-444397/37.
DR N-PSDB; AAX86987.
XX
XX
PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
PT in mammalian cancer cells.
XX
XX
PS Claim 1; Fig 1A; 86pp; English.
XX
XX

CC This sequence represents a novel human cytokine, designated Apo-2 ligand
CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
CC induce apoptosis for pathological conditions characterized by decreased
CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
CC coding sequence can also be used in quantitative and screening diagnostic
CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
CC associated with increased apoptosis
XX
XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAATYYVFTNELKOMODKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAATYYVFTNELKOMODKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQYKWLRLVLRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQYKWLRLVLRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
AAY81956
ID AAY81956 standard; protein; 281 AA.
XX AAY81956;
AC
XX 10-JUL-2000 (first entry)
DT
XX
DE Human Apo-2 ligand protein sequence.
XX
KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
KW therapy; apoptosis; cancer.
XX Homo sapiens.
XX US6046048-A.
PN
XX 04-APR-2000.
PD
XX 08-JAN-1997; 97US-00780496.
PF
XX 09-JAN-1996; 96US-0009755P.
PR
XX (GETH) GENENTECH INC.
XX
XX Kim KJ, Ashkenazi AJ, Chuntharapai A;
PI WPI; 2000-282690/24.
XX N-PSDB; AAA07425.
DR
XX
XX
PT New isolated monoclonal antibodies having antigen specificity for Apo-2
PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
PT -2 ligand serum, and for treating diseases associated with increased
PT apoptosis.
XX
XX Claim 9; Fig 1a; 46pp; English.
PS

This sequence is the human Apo-2 ligand protein, which is recognised by
monoclonal antibodies produced by the hybridoma cell lines of the
invention. The hybridoma cell lines are deposited under the American Type
Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
tissues, or serum. The antibodies may also be employed as therapeutics.
For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
pathological conditions or diseases associated with increased apoptosis.
They are also useful for the affinity purification of Apo-2 ligand from
recombinant cell culture or natural sources. The Apo-2 ligand itself may
be used to treat diseases e.g. cancer, by inducing apoptosis in cells
Sequence 281 AA;
SQ

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAATYYVFTNELKOMODKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAATYYVFTNELKOMODKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQYKWLRLVLRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQYKWLRLVLRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 10
AAB24038
ID AAB24038 standard; protein; 281 AA.
XX AAB24038;
AC
XX 25-JAN-2001 (first entry)
DT
XX
DE Human PRO1096 protein sequence SEQ ID NO:51.
XX
XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW identification; tumourigenesis; anticancer; detection.
XX Homo sapiens.
XX WO2000053750-A1.
PN
XX 14-SEP-2000.
PD
XX 02-DEC-1999; 99WO-US028551.
PF
XX 08-MAR-1999; 99WO-US005028.
PR
XX 01-SEP-1999; 99WO-US020111.
PR
XX 29-OCT-1999; 99US-0162506P.
PR
XX 30-NOV-1999; 99WO-US028313.
PR
XX 01-DEC-1999; 99WO-US028634.
XX
XX (GETH) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
PI WPI; 2000-594320/56.
XX N-PSDB; AAC58120.
DR
XX
XX
XX

Antibodies specific for PRO polypeptides, used to diagnose and inhibit
the growth of tumors in mammals, and to identify inhibitors of PRO
polypeptide activity or expression.
Claim 61; Fig 36; 226pp; English.
XX
XX The present invention describes an antibody that binds to a human protein
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
CC activity and can be used to diagnose tumours in mammals, by detecting
CC complex formation when the antibody is contacted with test cells.
CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially
CC the antibodies, or an antisense oligonucleotide which hybridises to genes
CC encoding (I), can be used to inhibit tumour growth, preferably by
CC inducing cell death. Methods from the present invention can be used to
CC identify compounds which inhibit the biological activity of (I). AAC58019
CC to AAC58102 represent PCR primers and hybridisation probes used in
CC examples from the present invention for human PRO sequences. AAC58103 to
CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
CC protein sequences given in the exemplification of the present invention
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGQTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYMDPNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYMDPNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSPDPILMKSARNSCWSDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSPDPILMKSARNSCWSDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 11
AAB08545
ID AAB08545 standard; protein; 281 AA.

AC AAB08545;
XX
DT 20-DEC-2000 (first entry)
XX
DE Amino acid sequence of a human TRAIL polypeptide.
XX
KW Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
KW TNF related apoptosis-inducing ligand; tumour cell;
KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
KW non-small cell lung carcinoma.
XX
OS Homo sapiens.
XX
PN WO200048619-A1.
XX
PD 24-AUG-2000.
XX
PF 15-FEB-2000; 2000WO-US003891.
XX
PR 16-FEB-1999; 99US-0120313P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Rosen GD;
XX
DR WPI; 2000-558253/51.
DR N-PSDB; AAA64325.
XX
PT Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
PT administration of synergistic combination of diterpenoid diepoxide and
PT tumor necrosis factor related apoptosis-inducing ligand.
XX

PS Disclosure; Page 23-24; 29pp; English.

XX
CC The present sequence represents a human TRAIL (tumour necrosis factor
CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
CC describes a method for enhanced killing of tumour cells. The method
CC comprises contacting a susceptible tumour cell with a synergistic mixture
CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
CC and so is active at lower doses and against otherwise resistant cell
CC lines. The method is used for killing tumour cells, especially solid
CC tumours or carcinomas (especially mammary carcinoma or non-small cell
XX lung carcinoma)

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGQTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYMDPNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYMDPNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSPDPILMKSARNSCWSDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSPDPILMKSARNSCWSDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 12
AAB28691
ID AAB28691 standard; protein; 281 AA.

AC AAB28691;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human AGP-1.
XX
KW Human; AGP-1; type II transmembrane protein; cytoslatic; antiviral;
KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200063253-A1.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008004.
XX
PR 16-APR-1999; 99US-00293245.
XX
PA (AMGE-) AMGEN INC.
XX
PI Hsu H, Meng S;
XX
DR WPI; 2000-665240/64.
DR N-PSDB; AAC67831.
XX

PT	Fusion protein of AGP-1 protein and an Fc region, used to treat
PT	proliferative disorders, immune disorders, and virally-induced disorders..
XX	
PS	Claim 3; Fig 2; 93pp; English.

The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an Fc immunoglobulin region fused to the N-terminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies

Sequence 281 AA;

Query Match	100.0%;	Score 1478;	DB 3;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 2.6e-137;		
Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MAMMEVQGGPSLGGTLCVLIVIFTVLLQSLCVAATVYVYFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGGTLCVLIVIFTVLLQSLCVAATVYVYFTNELKQMDKYSKSGIACFLKE 60

QY	61 DDSYMDPNDEESMNSPCWQVKWQLRQLVAKMLRTSEETISTVQEKQNISPLVRGPGQ 120
Db	61 DDSYMDPNDEESMNSPCWQVKWQLRQLVAKMLRTSEETISTVQEKQNISPLVRGPGQ 120

QY 121 RAAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 |||||
Db 121 RAAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

QY		181 FYYIYSQTFRFQOEIKENTKNDKOMQYIKYKTSYPDPILMLKSARNSCWSKDAAEGLY 240
Db		181 FYYIYSQTYFRFOEIKENTKNDKOMQYIKYKTSYPDPILMLKSARNSCWSKDAEGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 13
AAB50977
ID AAB50977 standard; protein: 281 AA.

XX	
AC	AAB50977;
XX	
DT	21-MAR-2001 (first entry)

XX Human PRO1096 protein.
DE
XX
KW Human; PRO; cyostatic; nootropic; neuroprotective; respiratory general;

OS Homo sapiens.
XX antiinflammatory; angiogenic; immunosuppressive; immunoregulatory;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX WO2000073348-A2.
PN
XX
PD 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US014941.
PF
XX
DB 03-TTN-1999. 99WO-US012252.

PR 23-JUN-1999; 99US-0141037F.
PR 20-JUL-1999; 99US-0144758F.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.

PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028634.
PR	02-DEC-1999;	99WO-US028551.
PR	09-DEC-1999;	99US-0170262P.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030999.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	18-FEB-2000;	2000WO-US004342.
PR	02-MAR-2000;	2000WO-US005841.
PR	03-MAR-2000;	2000US-0187202P.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.

PA (GETH) GENENTECH INC.

xx Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 pi Shelton DL, Smith V, Watanabe CK, Wood WI;

DR WPI; 2001-016509/02.

DR N-PSDB; AAC91579.

xx Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.

aa Claim 31; Fig 54; 188pp; English.
PS

The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoealic disorders, and inflammatory, angiogenic and immunological disorders

Sequence 281 AA;

Query Match	100.0%;	Score 1478;	DB 4;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 2.6e-137;		
Matches 281; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY      1 MAMMEVGGPSLGTCTVLIVIFTVLLQSLCVAATVYVFETNELKQMMDKYSKSGIACFLKE   60
        |||||
Db      1 MAMMEVGGPSLGTCTVLIVIFTVLLQSLCVAATVYVFETNELKQMMDKYSKSGIACFLKE   60
```

	61	DSYMDPNDDEESMNSPCWQVWKQLRQLVRKMLLRTSEETISTVQEKQNTISPLVRERGPQ	120
QY			
Dlb	61	DSYMDPNDDEESMNSPCWQVWKQLRQLVRKMLLRTSEETISTVQEKQNTISPLVRERGPQ	120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
|||||

Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
|||||

QY	181	FYYIYSQTYERFQOEIKENTKNDKQMWQIYKYTSYPDPILMLKSARNSCWSKDAEYGLY	240
Db	181	FYYIYSQTYERFQOEIKENTKNDKQMWQIYKYTSYPDPILMLKSARNSCWSKDAEYGLY	240

OY	241	SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFEQAFVLVG	281
Dh	241	SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFEQAFVLVG	281

RESULT 14
AAB67243
ID AAB67243 standard; protein; 281 AA..

Page 8

```
XX AC AAB67243;
XX DT 18-APR-2001 (first entry)
XX DE Human Apo2 ligand.
XX KM Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
XX OS Homo sapiens.
XX PN WO200100832-A1.
XX PD 04-JAN-2001.
XX PF 26-JUN-2000; 2000WO-US017579.
XX PR 28-JUN-1999; 99US-0141342P.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX DR WPI; 2001-123012/13.
XX PT Use of divalent metal ions for making Apo-2 ligand and in formulations
XX PT containing Apo-2 ligand for increasing yield and stability of ligand
XX PT trimers, useful for therapeutic applications.
XX PS Claim 6; Fig 1; 60pp; English.
XX CC The present invention relates to a formulation comprising Apo-2 ligand
XX CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
XX CC treating cancers and viral infections. Addition of divalent metal ions
XX CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
XX CC in increased yield and stability of Apo-2 ligand trimers
XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQWKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCQWKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 15
AAE11031
ID AAE11031 standard; protein; 281 AA.
XX
AC AAE11031;
DT 18-DEC-2001 (first entry)
XX
```

```
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
XX
XX KM Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
XX KM TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
XX KM human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
XX KM melanoma.
XX OS Homo sapiens.
XX FH Key
XX FH Domain
XX FT Location/Qualifiers
XX FT 1.18
XX FT /label= N_terminal_cytoplasmic_domain
XX FT Region
XX FT 19.38
XX FT /label= Transmembrane_region
XX FT Domain
XX FT 39.281
XX FT /label= Extracellular_domain
XX PN US6284236-B1.
XX PD 04-SEP-2001.
XX PF 26-MAY-1999; 99US-00320424.
XX PR 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX PR 25-JUN-1996; 96US-00670354.
XX PR 26-MAR-1998; 98US-00048641.
XX PR 10-NOV-1998; 98US-00190046.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Wiley SR, Goodwin RG;
XX DR WPI; 2001-595463/67.
XX DR N-PSDB; AAD18395.
XX PT New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX PT for treating viral infections (e.g. bovine viral diarrhea or human
XX PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX PS Claim 2; Col 45-48; 41pp; English.
XX CC The invention relates to a cytokine designated as tumour necrosis factor
XX CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX CC of certain target cells, including cancer cells and virally infected
XX CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
XX CC treating viral infections (e.g. bovine viral diarrhoea or human
XX CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
XX CC melanoma), as a research reagent useful in studying apoptosis including
XX CC the regulation of programmed cell death. TRAIL DNA sequences may be
XX CC employed in developing a gene therapy approach to treating disorders
XX CC mediated by defective or insufficient amounts of TRAIL, in the production
XX CC of TRAIL polypeptides and as probes or primers in polymerase chain
XX CC reactions (PCR). The present sequence is human TRAIL protein
XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQWKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCQWKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
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OY 181 FYYTYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
Db 181 FYYTYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
OY 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281
Db 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281

Search completed: September 5, 2004, 09:24:42
Job time : 73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:17 ; Search time 73 Seconds

(without alignments)
1212.785 Million cell updates/sec

Title: US-10-662-431-2

Perfect score: 1478

Sequence: 1 MAMMEVGGPSLGTCTVLIV.....NEHLIDMDHEASFGAPLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	US-08-916-625B-6	Sequence 6, Appli
2	1478	100.0	281	US-08-917-317A-8	Sequence 8, Appli
3	1478	100.0	281	US-09-813-329-17	Sequence 17, Appli
4	1478	100.0	281	US-09-193-663-8	Sequence 8, Appli
5	1478	100.0	281	US-09-934-465-1	Sequence 1, Appli
6	1478	100.0	281	US-09-919-039-118	Sequence 118, App
7	1478	100.0	281	US-10-202-062-20	Sequence 20, Appli
8	1478	100.0	281	US-10-662-429-2	Sequence 2, Appli
9	1478	100.0	281	US-10-662-430-2	Sequence 2, Appli
10	1478	100.0	281	US-10-662-431-2	Sequence 2, Appli
11	1478	100.0	281	US-10-652-244-2	Sequence 2, Appli
12	1478	100.0	281	US-10-279-687-8	Sequence 8, Appli
13	1478	100.0	281	US-10-039-785-66	Sequence 66, Appli
14	1478	100.0	281	US-10-011-125-4	Sequence 4, Appli
15	1478	100.0	281	US-10-001-054-54	Sequence 54, Appli

16	1478	100.0	281	14	US-10-093-766-54	Sequence 54, Appli
17	1478	100.0	281	14	US-10-174-654-11	Sequence 11, Appli
18	1478	100.0	281	14	US-10-151-882-41	Sequence 41, Appli
19	1478	100.0	281	14	US-10-218-547-20	Sequence 20, Appli
20	1478	100.0	281	14	US-10-322-673-72	Sequence 72, Appli
21	1478	100.0	281	14	US-10-139-785-66	Sequence 66, Appli
22	1478	100.0	281	14	US-10-310-793-26	Sequence 26, Appli
23	1478	100.0	281	15	US-10-292-486-5	Sequence 5, Appli
24	1478	100.0	281	16	US-10-381-160-5	Sequence 1, Appli
25	1478	100.0	281	15	US-10-333-712-1	Sequence 3, Appli
26	1469	99.4	279	13	US-10-066-209-3	Sequence 13, Appli
27	1269.5	85.9	246	9	US-09-855-544A-13	Sequence 16, Appli
28	1017	68.8	208	9	US-09-855-544A-16	Sequence 11, Appli
29	988	66.8	253	12	US-10-652-244-11	Sequence 13, Appli
30	988	66.8	256	12	US-10-652-244-13	Sequence 6, Appli
31	985.5	66.7	461	12	US-10-389-223A-6	Sequence 4, Appli
32	982	66.4	480	12	US-10-389-223A-4	Sequence 2, Appli
33	978	66.2	614	12	US-10-389-223A-2	Sequence 5, Appli
34	964.5	65.3	296	14	US-10-185-425-5	Sequence 14, Appli
35	937.5	63.4	188	9	US-09-855-544A-14	Sequence 6, Appli
36	930	62.9	291	10	US-09-873-829-6	Sequence 6, Appli
37	930	62.9	291	12	US-10-652-244-6	Sequence 6, Appli
38	930	62.9	291	13	US-10-017-910-6	Sequence 10, Appli
39	887	60.0	168	9	US-09-900-530A-10	Sequence 16, Appli
40	878	59.4	166	9	US-09-779-050A-16	Sequence 29, Appli
41	859	58.1	164	13	US-10-116-378-29	Sequence 7, Appli
42	850	57.5	161	14	US-10-216-074-7	Sequence 11, Appli
43	849	57.4	161	14	US-10-338-083-11	Sequence 17, Appli
44	636	43.0	172	9	US-09-779-050A-17	Sequence 15, Appli
45	561	38.0	113	9	US-09-855-544A-15	

ALIGNMENTS

RESULT 1
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 4
US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

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Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DDSYWDENDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREKGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSARNSCWSDAEYGLY 240
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RESULT 5
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US2002010223A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

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Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
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Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSARNSCWSDAEYGLY 240
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Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 6
US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 7
US-10-202-062-20
; Sequence 20, Application US/10202062

Publication No. US20040038349A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PF559
CURRENT APPLICATION NUMBER: US/10/202,062
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 281
TYPE: PRT
ORGANISM: human
US-10-202-062-20

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 8
US-10-662-429-2
Sequence 2, Application US/10662429
Publication No. US20040038347A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,429
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60

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61 DDSYMDPNDDEESMNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DDSYMDPNDDEESMNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHLRNGELVTHEKG 180
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHLRNGELVTHEKG 180

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240
181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTSYPDPILMK SARNSCWSKDAEYGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
US-10-662-430-2
Sequence 2, Application US/10662430
Publication No. US20040048340A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,430
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-10-662-430-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGPGSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGPGSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 10
US-10-662-431-2

; Sequence 2, Application US/10662431
; Publication No. US20040047864A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,431
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-662-431-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGPGSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 11
US-10-652-244-2

; Sequence 2, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-652-244-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGPGSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGPGSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

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Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY      181 FYIYSQTYFRFQOEIKENTKNDKQWQYIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
      181 FYIYSQTYFRFQOEIKENTKNDKQWQYIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
Db      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
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RESULT 12

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US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8
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Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
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      |||||||
Db      61 DDSYWDPNDEESMNSPCQVQWQOLRQLVRKMLIRTSEETISTVQEKQONISPLVREGPQ 120
QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
      |||||||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY      181 FYIYSQTYFRFQOEIKENTKNDKQWQYIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
      |||||||
Db      181 FYIYSQTYFRFQOEIKENTKNDKQWQYIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
QY      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
      |||||||
Db      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
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RESULT 13

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US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
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;; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66
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Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY      61 DDSYWDPNDEESMNSPCQVQWQOLRQLVRKMLIRTSEETISTVQEKQONISPLVREGPQ 120
      |||||||
Db      61 DDSYWDPNDEESMNSPCQVQWQOLRQLVRKMLIRTSEETISTVQEKQONISPLVREGPQ 120
QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
      |||||||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY      181 FYIYSQTYFRFQOEIKENTKNDKQWQYIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
      |||||||
Db      181 FYIYSQTYFRFQOEIKENTKNDKQWQYIYKTSYDPDILMKSAARNSCWSKDAEYGLY 240
QY      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
      |||||||
Db      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
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RESULT 14

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US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4
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Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMMEVQGGPSLQOTCVLIVIFTVLQSLCVAVTYVYFTNELKQWQDKYSKGIACFLKE 60
| | | | |
Db 1 MAMMEVQGGPSLQOTCVLIVIFTVLQSLCVAVTYVYFTNELKQWQDKYSKGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVKMLIRTSEETISTVQEKQONISPLVRERGPQ 120
| | | | |
Db 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVKMLIRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
| | | | |
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSA RNSCWSKDAEYGLY 240
| | | | |
Db 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSA RNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGATLVG 281
| | | | |
Db 241 SIYQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGATLVG 281

RESULT 15

US-10-001-054-54

; Sequence 54, Application US/10001054

; Publication No. US20020192209A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Baker, Kevin

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Hebert, Carolyn

; APPLICANT: Henzel, William

; APPLICANT: Kabakoff, Rhona

; APPLICANT: Shelton, David

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC

; TITLE OF INVENTION: CELL GROWTH

; FILE REFERENCE: P3034R1PCT

; CURRENT APPLICATION NUMBER: US/10/001,054

; CURRENT FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/079920

; PRIOR FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 60/082999

; PRIOR FILING DATE: 1998-04-24

; PRIOR APPLICATION NUMBER: 60/083545

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/085149

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/088858

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: 60/090691

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/096891

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: 60/096894

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: 60/099803

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/100263

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; PRIOR APPLICATION NUMBER: 60/100390

; PRIOR FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: 60/101476

; PRIOR FILING DATE: 1998-09-23

;; PRIOR APPLICATION NUMBER: 60/107783
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: 60/108849
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;; PRIOR FILING DATE: 2000-09-15
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;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: PCT/US99/05028
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PRIOR APPLICATION NUMBER: PCT/US99/08615
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
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PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-12-01
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PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-06
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PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
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PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 54
LENGTH: 281
TYPE: PRT

ORGANISM: Homo Sapien
US-10-001-054-54
Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCWQVKQDLRLVRKMLRTSEETISTVQEKQONISPLVREKGPQ 120
DB 61 DDSYWDNDDESMNSPCWQVKQDLRLVRKMLRTSEETISTVQEKQONISPLVREKGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSQHSFLSNLHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSQHSFLSNLHLRNGELVTHEKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYPDPILMKSARNSCWSKDAEYGLY 240
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DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

Search completed: September 5, 2004, 09:31:57
Job time : 74 secs